UNIVERSITY OF Hull

POP GROUP 44

Population Genetics Group

4-7 January 2011

Conference Programme

Welcome to
The 44th Population Genetics Group Meeting

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The organisers would like to thank the following sponsors for supporting this meeting:

General information

Accommodation is in the University of Hull's student residence at Thwaite Hall, which is set in 24 acres of grounds including the University's Botanic Gardens. The address is: Thwaite Street, Cottingham, North Humberside, HU16 4RE.

Registration will be held from 17.00 on Tuesday 4th January, in the main Foyer of Thwaite Hall. The bar will be open 17.00-01.00, and dinner will be available at Thwaite Hall 18.30-21.00. For those arriving during the daytime on Wednesday or Thursday, please make your way directly to the University. Late registration will be possible during coffee breaks in Staff House and you will be able to store your luggage.

Internet (wifi) facilities are available in Wilberforce lecture theatres and Staff house (coffee and lunch). You may join the eduroam network using your home university details, or usernames and passwords will be provided at registration. Thwaite Hall library and some other rooms are also covered by wifi.

Transport:

Buses leave every 20 to 30 minutes from Hull Paragon Interchange (combined train and bus station) to the University and Thwaite Street (for Thwaite Hall). Use bus numbers 63, 105, 115 or X47 (note, the 115 stops on Cranbrook Road for the University whereas the other 3 stop opposite the main entrance on Cottingham Road.

Taxis: For private taxis call 35 Taxis on (01482) 353535, Hull Cars on (01482) 828282 or Phoenix and Hessle Taxis on (01482) 654321.

Parking space is very limited at Thwaite Hall, but spaces will be available in the HYMS/HUBS car park of the University (see campus map). If you arrive by car on Tuesday, please make your way to Thwaite Hall and we will advise you on parking. A minibus will be available on Tuesday evening to shuttle delegates between the University car park and Thwaite.

Coaches will transport you from Thwaite Hall to the University and back, and from Thwaite to The Deep (for the conference dinner). Please see announcements at Thwaite for coach times.

Meals:

Breakfast will be at Thwaite Hall 07.15-08.15.

Coffee breaks will be held in the Lindsey Suite, Staff House (see University campus map)

Lunch will be 12.40-14.00 on Wednesday, Thursday and Friday in the Myton Servery at Staff House. Lunch vouchers, which entitle you to a main course and drink, can be found in your conference pack.

Evening meals will be served on Tuesday 18.30-21.00 and on Wednesday 19.30-21.00 at Thwaite Hall. Please see below for information on Thursday's conference dinner.

Bar facilities: A bar will be open in Thwaite Hall on Tuesday and Wednesday evenings until 01.00. Tea and coffee can be purchased from vending machines in the dining and common rooms.

Events:

Student welcome reception: A reception for students will be held in the games room at Thwaite Hall 8pm Tuesday 4th Jan.

Poster session: A dedicated poster session and wine reception will take place on Wednesday 17.00-19.00 in the Lindsey Suite at Staff House. Please make sure that you are stood by your poster during this time. Coaches will return to Thwaite Hall, after the poster session, for dinner.

Conference dinner: The conference dinner will take place on Thursday evening at The Deep. Coaches will depart from Thwaite Hall, with the first coach leaving at 18.15. We are operating a traffic light system to stagger arrival. Please see the notice boards in Thwaite for further information.

Business meeting: The PGG business meeting will take place at 17.00 on Wednesday in Wilberforce Lecture Theatre 1.

Talks and posters:

Talks will be held three lecture theatres (1, 2, 15 and 29) in the Wilberforce Building, University of Hull (see main campus map). Talks should be 15 minutes, with 5 minutes for questions. Please upload your talk onto the computer in the Lecture Theatre well before the start of the session. A helper will be present in the lecture theatres during breaks to assist you. Talks will be saved with the time of your talk followed by your surname (e.g. 1015 Smith.pptx) and filed in the folder appropriate to your session.

Plenaries will be held in Lecture Theatre 1 at 09.00. We would like to thank the Genetics Society for sponsoring the plenary sessions.

Chairs: The last speaker of each session should act as a chair for that session. If you are unable to do so, please notify one of the organisers as soon as possible.

Posters should be mounted in Lindsey Suite, Staff House, in time for the Poster Session (17.00 on Wednesday). The Lindsey Suite will be available during coffee and lunch breaks for poster mounting and viewing. Please leave your poster mounted for the duration of the conference, but make sure it is taken down by the end of Friday lunchtime.

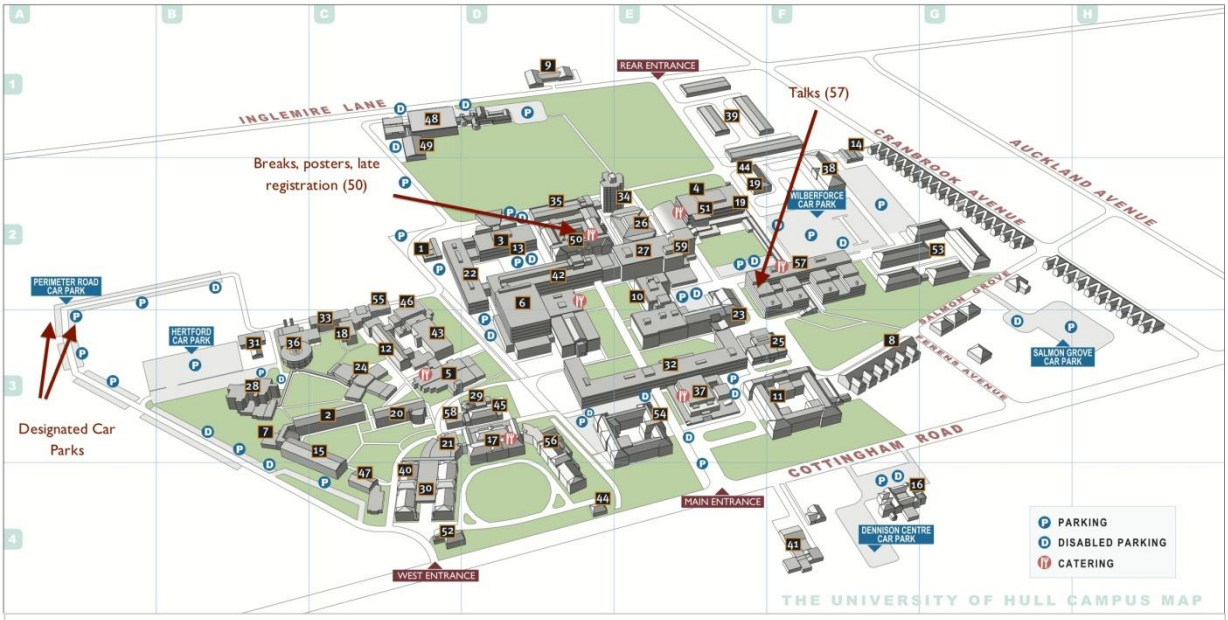
Prizes will be awarded at the conference dinner for the best student talks and posters. If you have been given a voting form in your conference bag, please return it to the box in Thwaite Hall, or to one of the organisers, by 18.00 on Thursday. We would like to thank the following sponsors for supporting the student prizes: Royal Society Publishing, Wiley Blackwell, Source BioScience Lifesciences, Oxford University Press and Roberts publishing.

Emergency Information:

In case of emergency at Thwaite Hall, please contact 07884 283274.

Hull Royal Infirmary is situated on Anlaby Road and has an A&E department. The infirmary is a taxi journey from the University and Thwaite Hall. There is a pharmacist on King Street, close to Thwaite Hall.

Campus map



Talks

Wednesday 5th January				
Time	LT1	LT2	LT15	LT29
08.55-09.00	Welcome & announcements			
09.00-10.00	Plenary Lecture: Gil McVean: Implications of the 1000 Genomes Project for human population genetics			
10.00-10.20	Kermit Ritland: Applications of genetical genomics	Warren Booth: Genetic Evidence for Facultative Parthenogenetic Reproduction in Squamate Reptiles.	Linliang Wang: Estimating selfing rates from multilocus genotype data	Frank Shaw: The contrasting roles of seed and pollen migration in niche evolution.
10.20-10.40	Richard Nichols (chair): Characterising genetic diversity in the world of next generation sequencing	Jacob Höglund (chair): Detecting hybridization between willow grouse (*Lagopus lagopus*) and rock ptarmigan (*L. muta*) in Central Sweden through Bayesian admixture analyses and mtDNA screening	Bjarki Eldon (chair): Concordance between species trees and gene genealogies with multiple mergers	Sean Hoban (chair): Human impacted landscapes facilitate hybridization between a native and an introduced tree
10.40-11.20	Break			
11.20-11.40	[S]Andrea Simon: Single introduction of topmouth gudgeon into Europe from an admixed source population followed by long-distance dispersal	[S]Thomas Mathers: Multiple evolutions of alternative reproductive modes in tadpole shrimps	Jitka Polechová: Drift widens the expected cline but narrows the expected cline width	Paris Veitsos: Selection and population differentiation for song and cuticular hydrocarbons in *Drosophila montana*
11.40-12.00	[S]Cathleen Thomas: The Global Invasion of the Harlequin Ladybird (*Harmonia axyridis*)	[S]Crispin Jordan: The potential for intralocus sexually antagonistic polymorphism among genomic regions	[S]Suo Qiu: Patterns of codon usage bias in *Silene latifolia*	Stuart Baird: Decay of reproductive isolation in the European house mouse hybrid zone: empirical evidence and a model
12.20-12.20	Tamsin Majerus: The Evolutionary Consequences of Male-killing: Sex and Ladybirds!	[S]Juanita Olano-Marin: Correlations between heterozygosity and reproductive success in the blue tit (*Cyanistes caeruleus*)	[S]Guillaume Achaz: How epistatic chains constraints the order of mutations.	[S]Paul Nichols: The effect of gene-flow at a secondary contact zone on hybrid morphology in the cichlid fish *Astatotilapia calliptera*
12.20-12.40	[S]James Buckley (chair): Evolutionary change in host plant preference associated with the northward range shift of the Brown Argus butterfly	Patricia Brekke (chair): Promiscuity as a strategy for avoiding inbreeding by an island bound species.	Nick Priest (chair): The role of compensatory mutation in the evolution of gene regulatory networks	Catherine Cullingham (chair): Genetically informed species distributions across a hybrid zone (lodgepole pine × jack pine) in central Alberta, Canada
12.40-14.00	Lunch			
14.00-14.20	Isa-Rita Russo: Mitochondrial DNA differentiation within the Eastern Kalahari Bushveld lineage of *Micaelamys namaquensis* (Rodentia: Muridae)	[S]Stephen Moss: Comparative analysis of teleost fish genomes reveals novel patterns of intron size distribution	[S]Robert Donnelly: Molecular and morphological variation within the sentinel species, *Lumbricus rubellus*	
14.20-14.40	[S]Mafalda Costa: Mitochondrial DNA variation and population structure of polecats and ferrets in the British Isles	Christian Schlötterer: DNA double-strand break repair and the evolution of intron density	[S]Toni Gossman: Quantifying the variation in the effective population size within a genome.	
14.40-15.00	[S]Gil Smith: Using a multi locus approach to infer the phylogeography of *Drosophila mojavensis*	Martin Carr: Phylogenomics of Ty LTR retrotransposons in *Saccharomyces cerevisiae*	[S]Marco Andrello: Contrasting estimates of effective population size based on demographic and genetic data in *Eryngium alpinum* L. (Apiaceae).	
15.00-15.20	Xiangjiiang Zhan (Chair): Molecular phylogeography of the blood pheasant	Chris Wheat (chair): Dating the models: arthropod macroevolutionary events and a revision of model genomic species' divergences	Konrad Lohse (chair): Generating functions for the structured coalescent	
15.20-16.00	Break			

Note, "S" denotes a student talk

Wednesday 5th January, cont.

16.00-16.20	**Joram Mwacharo**: Pattern of chicken domestication and dispersion in the Old World: A Bayesian perspective	[s]**Richard Merrill:** It's a kind of magic: Ecological speciation in *Heliconius* butterflies	**Seirian Sumner:** Transcriptome analyses reveal that worker behaviour in a eusocial wasp originates by delaying social maturation
16.20-16.40	[s]**Vera Warmuth:** The relative roles of demic diffusion and local recruitment in the spread of horse domestication	[s]**Aliya El Nagar:** Parasites in ecological speciation; heritability of parasite resistance in the three-spined stickleback	[s]**Ian Williams:** Investigating the mating success of honeybee queens in a managed apiary in mid-Wales
16.40-17.00	[s]**Simon Aeschbacher (Chair):** The fate of a domesticated allele in the wild: inference based on a drift-migration-selection model	**Irene Keller (chair):** Gene flow constrains adaptive divergence between trout populations	**Rob Hammond (chair):** Evolutionarily labile social organisation in an ant
17.00-19.00	Business meeting, Poster session and wine reception		

Thursday 6th January			
Time	**LT1**	**LT2**	**LT15**
08.55-09.00	Announcements		
09.00-10.00	**Plenary Lecture: Eske Willerslev:**		
10.00-10.20	[S]**Lucy Gattepaille:** Combining markers into haplotype can improve population structure inference	**Kate Ciborowski:** Temporal genetic variation within and among wild populations of Atlantic salmon	[S]**Hildegard Uecker:** On the fixation process of a beneficial mutation in a variable environment
10.20-10.40	[S]**Robert Verity (chair):** A Modern Perspective on Measures of Population Differentiation	**Bill Jordan (chair):** Morphological and Genetic Differences Between Pelagic and Benthic of Arctic Charr	**Gael Raoul (chair):** Analysis of a model introduced by Kimura.
10.40-11.20	**Break**		
11.20-11.40	**Per Sjodin:** No evidence for ancient bottleneck in African human populations	**Alexia Massa-Galluc:** Unraveling patterns of genetic diversity in a salmonid metapopulation	**Jerome Kelleher:** Recombination in the extinction/recolonisation model
11.40-12.00	[S]**Flora Jay:** Predictions of Native American population structure using languagecovariates in a hidden regression framework	[S]**Sara Vandamme:** Genetic stock structure as a base for management. The case of turbot	[S]**Matthew Hartfield:** Recombination and the Undesirable Hitchhiker
12.20-12.20	[S]**Maria Warnefors:** Human genes have not reached their full regulatory potential	**Wilsea Figueiredo Ready:** Population structure in a migratory freshwater fish of the genus *Prochilodus*	**Daniel Weissman:** Dynamics of adaptation in large sexual populations
12.20-12.40	**Nina Stoletzki (chair):** The evolution of PRDM9 binding motifs in the human genome	**Mark Coulson (chair):** The use of genetic parentage analysis to assess the effectiveness of hatchery practice in a wild Atlantic salmon river.	**Len Nunney (chair):** The maintenance of sex - was Fisher right?
12.40-14.00	**Lunch**		
14.00-14.20	[S]**Daniel Jeffares (chair):** Searching for consistent signals of balancing selection in *Plasmodium falciparum* genes.	[S]**Mrinalini:** Species delimitation using AFLPs: A comparative methodological assessment	[S]**Tanja Strand:** Neutral (SNP) vs. adaptive (MHC) genetic diversity in black grouse populations of various degrees of isolation.
14.20-14.40	[S]**Colin McClure:** The Role of Pathogens in Ageing	[S]**Anja Marie Westram:** Discovering hidden biodiversity - population genetics of cryptic *Gammarus fossarum* species	[S]**Athanasios Kousathanas:** Positive and negative selection on non-coding DNA upstream and downstream of protein-coding genes in wild house mice
14.40-15.00	**Surendra Kumar Prajapati:** Age of the extant human malaria parasite *Plasmodium vivax*	[S]**Abhilash Nair:** Cryptic diversity of endemic Indirana frogs of the Western Ghats biodiversity hotspot	[S]**Kang-Wook Kim:** Genetic basis of the Gouldian finch (*Erythrura gouldiae*) colour polymorphism
15.00-15.20	**Roman Biek:** Integrating landscape genetics of a viral parasite and its vertebrate host	**Stefano Mariani (chair):** Sex ratio fluctuations favour the evolution of sex-changing strategies	**Annika Noreen (chair):** Higher-than-expected genetic diversity and potential genetic adaptability in the reef coral *Pocillopora damicornis* at a high latitude region**.**
15.20-16.00	**Break**		

Thursday 6th January cont.

16.00-16.20	[S]**Lewis Spurgin:** Patterns of MHC diversity in the early stages of divergence: insights from an endemic island bird	**Lucy Woodall:** Population genetics and phylogeography of the long-snouted seahorse *Hippocampus guttulatus*: The use of genetic tools in marine conservation	[S]**Iris Fischer:** Adaptation to drought in two wild tomato species: the evolution of the *Asr* gene family
16.20-16.40	[S]**Mark McMullan:** Spatial and temporal variation at the Major Histocompatibility Complex (MHC) in Trinidadian guppy populations	**Alison Thomas:** Genetic Differentiation of the Twin Spotted Wainscot Moth (*Archanara geminipuncta*) in UK *Phragmites* reedbeds	[S]**Pablo Orozco-ter Wengel:** Genomewide signatures of adaptation in *Drosophila melanogaster*
16.40-17.00	**Violaine Llaurens (chair):** Persistence of polymorphism in MHC Class II of guppy (*Poecilia reticulata*) may not rely on parasite mediated selection only.	**Rob Pickles (chair):** Using phylogeography to prioritise conservation effort in the giant otter	[S]**Martin Kapun (chair):** Experimental evolution of temperature adaptation in *Drosophila simulans*
18.15-late	**Conference Dinner**		

Friday 7th January

Friday 7th January			
Time	**LT1**	**LT2**	**LT15**
08.55-09.00	**Announcements**		
09.00-10.00	**Plenary Lecture: Jon Slate:** The genetics of conspicuous polymorphisms in Soay sheep		
10.00-10.20	**John Davey:** RAD Sequencing: A Method for Population Genomics	**Andrea Betancourt:** Molecular evolution of a Y chromosome to autosome gene duplication in *Drosophila*	**Brian Charlesworth:** Ancestral polymorphisms in two species of *Drosophila*
10.20-10.40	**Maureen Liu (chair):** RAD Genotyping Facilitates Rapid Marker Discovery in Species Without a Reference Genome	**Roberta Bergero (chair):** Evolution of sex chromosomes: insights from a dioecious plant	**Penny Haddrill (chair):** Determinants of Synonymous and Nonsynonymous Variability in Three Species of *Drosophila*
10.40-11.20	**Break**		
11.20-11.40	**Simon Creer:** Massively parallel biodiversity identification using "second generation" molecular ecology	**John Turner:** Why species have an edge.	**Sylvain Billiard:** Dynamics of diversification by coevolution: the case of the self-incompatibility locus
11.40-12.00	**Robert Ekblom:** Next generation sequencing in non-model organisms: A case study of the Ruff (*Philomachus pugnax*)	**Laurence Cook:** Melanic peppered moths: the end of the affair	**Luis-Miguel Chevin:** Some evolutionary demographic consequences of phenotypic plasticity
12.20-12.20	**Anna Santure:** Characterisation of the transcriptome of a wild bird, the great tit (*Parus major*), using next generation sequencing	**Adam Eyre-Walker (chair):** Does it matter where we publish?	**Kai Zeng:** The effects of demography and linkage on the estimation of selection and mutation parameters
12.20-12.40	**Anita Malhotra (chair):** Evolution of hypervariability in phospholipase A2 toxins from snake venoms		**Ruth Shaw (chair):** The distribution of genetic effects on fitness
12.40-14.00	**Lunch**		
Departure			

Plenary Lectures

Wednesday 5th January

Implications of the 1000 Genomes Project for human population genetics

Gil McVean

Oxford University, UK

The 1000 Genomes Project aims to provide a catalogue of human genomic variation by sequencing individuals from multiple populations across the world. While the focus of the project is on medical genetics, the data have the potential to tell us much about human population genetics. I will discuss findings from the project in two areas - the hunt for the genetic changes underlying human adaptation and our understanding of genetic differentiation between populations. I will also talk about the challenges of population genetic analysis from whole genome sequencing.

Thursday 6th January

Hunting the Molecular Past

Eske Willerslev

National History Museum of Denmark

In the past two decades, ancient DNA research has progressed from the retrieval of small fragments of mitochondrial DNA from a few relatively young specimens, to large-scale studies of ice age populations and whole genome sequencing of an ancient human. Recent methodological advances include DNA preserved in ancient hair shafts, coprolites, sediments, and ice. Coupling these with second generation sequencing technologies ancient DNA has positioned itself as a powerful tool in archaeology, paleontology, ecology and population genetics. Recent breakthroughs include evidence for human occupation in southwestern North America as early as 14,000 years ago (pre-Clovis), a previously unrecognized human migration from the Siberia to the New World around 5,500 years ago, the survival of mammoth and horse in central Alaska to at least 10,500 years ago – long after human arrival, and population dynamics underlying extinction of the ice age megafauna.

Friday 7th January

The genetics of conspicuous polymorphisms in Soay sheep

Jon Slate

University of Sheffield, UK

Identifying the molecular basis that causes phenotypic variation is a critical step in understanding how genetic variation is maintained. In this talk I will present work on the genetics of three single locus polymorphisms in a wild population of Soay sheep, on St Kilda, Scotland. The population is one of the most intensively studied mammal populations in the world; this, combined with a dramatically fluctuating population size makes Soay sheep an excellent system for studying selection and evolution in the natural environment. The genetics of three polymorphic traits, coat colour, coat pattern and horn type have now been resolved to the level of individual genes (and sometimes individual mutations), and in all three cases the ability to distinguish between sheep with similar phenotypes but different underlying genotypes has given new insight into how the polymorphisms are maintained. A major challenge will be extending this approach to the study of traits with a more complex genetic basis.

Talk Abstracts

How epistatic chains constraint the order of mutations.

Guillaume Achaz, D. Weinreich, Y. Kobayashi, A. Yamauchi & F. Tajima

Université Pierre & Marie Curie, Paris-6, France

At the genome scale, most of the genetic locus have interactions with other locus within the same genome. Using fitness landscape models, we show that allelic replacement at one locus can drive the allelic replacement at another interacting locus, which itself can drive another replacement at a third locus, etc. creating a "chain" of allelic replacements. This chain is a very strong constraint on the mutations order, since it predicts the order of several successive replacements. We show that incompatibilities between alleles at different interacting locus is a sufficient condition to observe such a chain. We also studied a "real" fitness landscape and show that epistatic chains do exist in nature.

The fate of a domesticated allele in the wild: inference based on a drift-migration-selection model

Simon Aeschbacher, Christine Grossen, Iris Biebach, Lukas F. Keller & Nick H. Barton

University of Edinburgh/ Institute of Science and Technology, Austria

We show evidence for selection on a Major Histocompatibility Complex (MHC) class II allele that supposedly introgressed from domestic goat (*Capra aegagrus hircus*) into a wild relative, the Alpine ibex (*C. ibex*). Genetic variation in MHC is high in most mammals, and balancing selection has been proposed as an explanation. Two competing hypotheses are overdominance versus negative frequency-dependent selection. In the spatially structured population of Alpine ibex we studied, however, diversity at the MHC is relatively low. We set up a drift-migration-selection model and numerically iterated the transition matrices to obtain joint and marginal likelihoods of parameters. In principle, the allele frequency data are compatible with various dominance schemes and, therefore, a wide range of selection coefficients. Considering additional short term signals of selection, we conclude that the introgressed allele has likely been under spatially homogeneous selection (Ne*s ~ 1 to 100), and that there is either underdominance or directional selection against it. These findings are compatible with frequency dependent selection, if we assume that we sampled in an area and at a time in which the 'goat' allele is disfavoured. Migration tends to reduce estimated selection coefficients, but cannot explain the data equally well on its own.

Contrasting estimates of effective population size based on demographic and genetic data in *Eryngium alpinum L.* (Apiaceae).

Marco Andrello, Myriam Gaudeul, Irène Till-Bottraud, & Oscar E. Gaggiotti

Université de Grenoble, France

Effective population size Ne is a central parameter in evolutionary biology and conservation. The estimation of Ne can be performed using demographic and genetic methods but estimates from the two approaches have rarely been compared. We estimated Ne in four populations of the endangered perennial plant *Eryngium alpinum* using one demographic and two genetic methods. Estimates from the three methods were very different (up to three orders of magnitude) and the discrepancies could be attributed to: lack of sufficient data needed to parameterize the demographic model; unknown performance of genetic estimators in relation to sample size and locus polymorphism; potential violations of model assumptions. Some issues arising when comparing different methods are also discussed: time period of applicability of the estimates; convergence to the stable-stage structure in populations with overlapping generations; which processes are and are not modelled in the demographic estimators. Although not strictly an estimation method, the demographic approach is a useful tool to understand the role of different factors (survival and fecundity rates, mating system, etc.) on Ne. The discrepancies observed in the present paper call for increased attention and additional studies comparing demographic and genetic approaches to the estimation of Ne.

Decay of reproductive isolation in the European house mouse hybrid zone: empirical evidence and a model

Stuart J.E. Baird, Milos Macholan, Pavel Munclinger, Joelle Gouy de Bellocq & Jaroslav Pialek

CIBIO, University of Porto, Portugal

The invasion of a Y chromosome across the Czech/Bavarian portion of the European mouse hybrid zone, accompanied by a distortion in the sex ratio, and in apparent disregard of Haldane's rule, seems strong empirical evidence of a local decay in reproductive isolation between taxa. Such decay may inform us about the balance of forces acting on the evolution of reproductive isolation. In the Y invasion case we have suggested genetic conflict may outweigh heterogametic incompatibility. Recent work on competition between trains of related sperm in rodents motivates a simple model of intra-ejaculate sperm competition. This simplicity allows analysis in combination with a simple model of heterogametic disadvantage. Numerical results in the one dimensional deterministic case show feasible amounts of genetic conflict can overcome considerable heterogametic disadvantage, allowing Y chromosome invasion. The predicted relative invasion pattern of X, Y and Mt markers allows model scenarios similar to the empirical data to be distinguished. We discuss whether and how such models might be used to infer the balance of forces acting on the evolution of reproductive isolation in the mouse hybrid zone.

Morphological and genetic differences between pelagic and benthic of Arctic charr

Kimberly Ballare, Samuel Martin, Johanna Slothouber Galbreath, Derek Pretswell, Ronald Greer & William Jordan

Institute of Zoology, London, UK

In many lakes Arctic charr (*Salvelinus alpinus*) exhibit a niche separation into pelagic and benthic forms. As well as occupying different positions in the water column the forms have been shown to have different diets and parasite loads. Here, we sampled Arctic charr from 4 polymorphic and 3 monomorphic lochs in Scotland. We carried both morphometric and genetic analyses on these samples. An objective analysis of morphological differences confirmed a subjective classification of the samples into pelagic and benthic forms. Furthermore, while the pelagic forms seemed similar to each other regardless of loch of origin, benthic fish seemed different from both pelagic fish and benthic samples from another loch. Patterns of mitochondrial variation showed no evidence that the forms arose through invasions from different glacial refugia but microsatellite variation suggested that the pelagic and benthic forms evolved in situ.

Generating functions for the structured coalescent

Nick H. Barton & Konrad Lohse

University of Edinburgh, UK

Analysis of genomic data requires an efficient way to calculate likelihoods across very large numbers of loci. We set out a general method for finding the distribution of genealogies; we allow migration between demes, splitting of demes (as in the IM model), and recombination between linked loci. These processes are described by a set of linear recursions for the generating function of branch lengths. Under the infinite-sites model, the probability of any configuration of mutations can be found by differentiating this generating function. Such calculations are feasible for small numbers of sampled genomes. Given data from a large number of non-recombining blocks, the likelihood can be calculated by tabulating the probabilities of all relevant mutational configurations, and then multiplying across loci.

The evolution of sex chromosomes: insights from a dioecious plant

Roberta Bergero, Suo Qiu & Deborah Charlesworth

University of Edinburgh, UK

According to the theory of sexual antagonism, sex chromosomes can become enriched for polymorphic genes that affect male and female fitness in opposite directions. Such genes are particularly expected in the pseudoautosomal region, and may lead to suppression of X-Y recombination. The plant *Silene latifolia* represents a good species for testing such expectations, because its sex chromosomes evolved recently, and non-dioecious *Silene* species can be used for comparative studies of gene content and synteny. Through linkage and sequence diversity analyses, six pseudoautosomal genes were identified, spanning a region of ~ 20-25 cM. Some of these genes have highly divergent alleles, possibly maintained by balancing selection, though it is unknown whether they have sexual antagonistic effects. Synteny was found between genes on the *S. latifolia* X chromosome and genes on a single linkage group of the non-dioecious *S. vulgaris*. However, genes close to the pseudoautosomal boundary do not map to the *S. vulgaris* linkage group homologous to the *S. latifolia* X chromosome. These findings show that, after recombination suppression leading to the initial differentiation of sex chromosomes from a pair of autosomes, further evolution of the sex chromosomes has involved translocations at the pseudoautosomal boundary, and the formation of a neo-X.

Integrating landscape genetics of a viral parasite and its vertebrate host

Roman Biek, David Wheeler & Lance Waller

University of Glasgow, UK

Landscape genetics seeks to describe how environmental variability shapes the genetic population structure of species. Despite large methodological advances in this area in recent years, it often remains ambiguous whether the inferred patterns of subdivision are really attributable to landscape effects. Independent verification could be achieved by examining genetic data from a separate species that is likely to respond to environmental variation in a similar fashion. Directly-transmitted parasites associated with the host species of interest are obvious candidates but have rarely been used in this context. Here, we apply novel analytical tools to data from a feline RNA-virus and its natural host, the cougar, to test whether both species show congruent patterns with respect to landscape features. Whereas previous analyses found pronounced genetic structure in the virus but not the host, our current results based on a Bayesian spatial clustering method for geo-referenced samples suggest a clear subdivision of cougar populations. Importantly, we find that viral movement across this putative barrier is very small compared to that for a set of equivalent random subdivisions. This demonstrates that integrating population genetic data from parasite and host can identify biologically meaningful boundaries to gene flow at the landscape scale.

Genetic Evidence for Facultative Parthenogenetic Reproduction in Squamate Reptiles.

Warren Booth, Gordon W. Schuett, Daniel H. Johnson, Sharon Moore, Coby Schal & Edward L. Vargo

North Carolina State University, USA

Parthenogenesis in vertebrates is considered an evolutionary novelty, reported in less than 0.1% of all species. In snakes, all of which exhibit genetic sex determination with ZZ:ZW sex chromosomes, although rare, an extraordinary diversity of parthenogenetic mechanisms have been described. Within the Macrostomata (i.e. advanced snakes), parthenogenesis has been reported within each of the three super-families (Pythonidae, Caenophidia, Boidae), with the viability, sex, and genetic makeup of the resulting offspring differing between each super-family. Through microsatellite DNA fingerprint, we describe two unique cases of parthenogenesis in snakes. Within the super-family Boidae, in a Boa constrictor, we describe the first evidence of multiple, viable, non-experimentally induced female offspring for the first time in any vertebrate lineage. In contrast, within the Caenophidia, we describe the first evidence of parthenogenesis within a North American pitviper, *Agkistrodon contortrix*, resulting in multiple male offspring. In both instances, automictic terminal fusion is expected. These results suggest that previous reports of long-term sperm storage within the squamata may in fact represent further instances of facultative parthenogenesis.

Promiscuity as a strategy for avoiding inbreeding by an island bound species.

Patricia Brekke

Institute of Zoology, London, UK

In closed populations, where options for dispersal are limited and relatives encounter one another frequently, the need to evolve kin recognition and the pre or post-copulatory stage is predicted to arise to avoid inbreeding and its deleterious fitness consequences. The island bound endemic New Zealand hihi (*Notiomystis cincta*) has a socially monogamous mating system with high rates of extra-pair paternity, making it a prime candidate to understand the effects of relatedness on mate choice in a spatially limited environment. I show that: (i) social mate choice is random with respect to relatedness in this species; (ii) relatedness levels of extra-pair matings are significantly lower than random; and finally (iii) the number of extra-pair male sires, or the proportion of extra-pair offspring per clutch, is not related to the social pair's relatedness level. I discuss how EPP, as an inbreeding avoidance mechanism, has potentially evolved in this species as a consequence of high encounter rates and few dispersal possibilities due to being bound to small islands or due to post-copulatory selection for more genetically compatible individuals.

Evolutionary change in host plant preference associated with the northward range shift of the Brown Argus butterfly

James Buckley & Jon Bridle

University of Bristol, UK

Recent climate change has driven rapid northward range expansion of the Brown Argus butterfly (*Aricia agestis*) in the UK by around 200km over the past 30 years. This range expansion appears to have involved a shift in host plant preference from the locally abundant host plant in long-established sites (predominately *Helianthemum nummularium*, but occasionally *Geranium* spp.) to exclusively *Geranium* spp. in the recently-colonised sites irrespective of local host plant abundance. Has there been evolutionary change in host plant preference associated with this northward range expansion? We will present evidence from assays of host plant preference and field reciprocal transplants that suggest there has been evolutionary change in host preference and discuss the potential consequences of this for continued responses to climate change in the future.

Phylogenomics of Ty LTR retrotransposons in *Saccharomyces cerevisiae*

Martin Carr

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Saccharomyces cerevisiae was the first eukaryote to have its genome completely sequenced, allowing the study of the evolution of its five known transposable element families (Ty1-Ty5). All five families are long terminal repeat (LTR) retrotransposons; Ty1-Ty3 are known to be transpositionally competent, while Ty5 is a non-transposing inactive family. We report here a re-analysis of the reference genome showing that previous studies have underestimated the copy number of each family. In addition, we have identified a sixth family of LTR retrotransposons composed entirely of solo LTRs. Phylogenetic analyses of whole genome data for each family identified short-branch putatively active clades nested within long branch presumably inactive elements. Population genomic data from 38 strains of *S. cerevisiae* show that elements present in the active clades are predominantly polymorphic, whereas most older elements are fixed.

Ancestral polymorphisms in two species of Drosophila

Brian Charlesworth, Reuben Nowell & Penelope Haddrill

University of Edinburgh, UK

Ancestral polymorphisms are that arose by mutation prior to the speciation event that generated the species in which they segregate. Their presence may complicate the interpretation of sequence divergence and lead to incorrect phylogenetic inferences. They may also be used to identify regions of the genome that may be under balancing selection. We extend a method for estimating the proportion of ancestral polymorphisms within species, and apply it to a dataset of nearly 70 protein-coding genes for which sequence polymorphism data is available in both *Drosophila pseudoobscura* and *D. miranda*, using *D. affinis* as an outgroup. We show that a substantial proportion of the synonymous variants in these two species are ancestral, and that a small number of genes with unusually high sequence diversity seem to show evidence of an excess of ancestral polymorphisms, suggestive of balancing selection.

Some evolutionary demographic consequences of phenotypic plasticity

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Phenotypic plasticity, the direct response of individual phenotypes to their environment of development, is increasingly considered a substantial component of phenotypic change and geographic variation in the wild. It should thus strongly affect how evolutionary and demographic processes interact in temporally changing or spatially heterogeneous environments. We investigate this for quantitative traits with linear reaction norms, where reaction norm slope quantifies the level of plasticity. We first study evolutionary recovery after an abrupt environmental shift initially causing population decline and extinction risk. Initial (partially adaptive) plasticity reduces the effective magnitude of the environmental shift, while evolution of plasticity increases the rate of adaptation. Therefore the minimum size of a population that can persist deterministically decreases exponentially with variance in plasticity, which can offset the impact of density dependence on population decline. We then turn to the evolution of plasticity in a sink population receiving immigrants from a larger source population. Maladaptation due to gene-flow causes higher plasticity to evolve in the sink at migration-selection equilibrium. The same occurs at edges of a continuous species range, but only with a cost of plasticity. Plasticity also can produce higher mean fitness and larger population size in sinks, facilitating invasion of new habitats.

Temporal genetic variation within and among wild populations of Atlantic salmon

Kate Ciborowski, Sofia Consuegra, Carlos Garcia de Leaniz, Jinliang Wang, Mark Beaumont & William Jordan

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Abstract not provided

Melanic peppered moths: the end of the affair

Laurence Cook, talk will be delivered by John Turner

Manchester Museum

In the 19th and 20th centuries increases in frequency of melanic morphs *carbonaria* and *insularia* in the peppered moth *Biston betularia* occurred in Britain, continental Europe and America in step with changing patterns of industrialization. Accounts of the early change are largely anecdotal but there are better quantitative records of the more recent decreases in frequency. These are reviewed to show rate of decline, geographical variation in rate and estimated fitness differences. The roles migration and of *insularia* alleles in determining overall change in melanic frequency are considered. Movement has played an important part in determining patterns.

Mitochondrial DNA variation and population structure of polecats and ferrets in the British Isles

Mafalda Costa, Carlos Fernandes, Margarida Santos-Reis & Michael W. Bruford

Cardiff University, UK

The polecat is experiencing a population decline in most European countries. Major threats include habitat destruction, direct persecution, and hybridisation with ferrets. Conversely, it is now known that the British polecat population is expanding its range after near-extinction in the 19th century. Here we present the results of preliminary analyses concerning the genetic variation and population structure of polecats and ferrets across the British Isles using mitochondrial control region sequences and 12 microsatellites. We estimated molecular diversity, population genetic structure and searched for signatures of population bottlenecks and expansions using haplotype and allele frequencies and Bayesian analysis. We are also examining patterns of introgression in UK and Portuguese polecat and ferrets. Genetic variation was found to be low and there was some evidence for a recent bottleneck in the UK sample. Results of introgression studies are ongoing and preliminary evidence will be presented.

The use of genetic parentage analysis to assess the effectiveness of hatchery practice in a wild Atlantic salmon river

Mark W Coulson, Lucy M. I. Webster, Anja A. Armstrong, , Robert Laughton & Eric Verspoor

RAFTS/Marine Scotland, UK

The use of hatcheries to support or enhance fish populations is a common practice, however the effectiveness of such operations is rarely documented. By applying genetic parentage analysis to rod caught fish returning to a river, supplemented with genetic information from the broodstock, we screened fish for evidence of having originated from the hatchery. In addition to genetic samples from the broodstock collected over 6 years, we have detailed breeding records of the specific crosses made in the hatchery. These records enhance the certainty of genetic parentage assignments by confirming that putative mothers and fathers of a given offspring were in fact involved in a spawning event. In addition to identifying a small proportion of rod-catch as hatchery-offspring, we identified several cases of broodfish from our most recent years as offspring of previous years' broodstock. Furthermore, we screen a small number of adults returning to a dam in the upper part of the catchment, above which stocking has taken place in the past. Genetic parentage analysis can allow for accurate calculations on the economics of running a hatchery and provide insight into the relative success of hatchery-reared vs. wild fish.

Massively parallel biodiversity identification using "second generation" molecular ecology.

Simon Creer

Bangor University, UK

Taxon assessment is the key to understanding the relationship between biodiversity and ecosystem processes, but the identification of microbial eukaryotes is impeded by a number of logistical and taxonomic factors. However, the most important restricting factor confounding the ecological research of any microbial community is the mismatch between diversity and the number of ecologists that are able to simultaneously identify and catalogue inter-phylum diversity. Contemporary pyrosequencing offers a solution to this problem in the form of environmental metagenetic analyses, but this represents a novel field of biodiversity assessment. Here, we cover some of the pros and cons of 454 Roche environmental metagenetic sequencing analyses via reference to example datasets derived from novel bioinformatic analyses of over 1 million nuclear small subunit 18S (nSSU) sequence reads of the meiofaunal biosphere. Comprised of between 50% (shallow water) and 90% (deep water) nematodes, meiofaunal assemblages contribute significantly to bentho-pelagic coupling in the form of nutrient cycling, water column processes, pollutant distribution, secondary production and stability of sediments. The data provide quantitative, objective and revealing insights into the relative magnitude, composition and identity of the meiobenthic biosphere in marine and estuarine environments.

Genetically informed species distributions across a hybrid zone (lodgepole pine × jack pine) in central Alberta, Canada

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University of Alberta, Canada

Hybridization among closely related species can be a complex process, and the first step toward understand this process is to distinguishing hybrids from their parentals and defining the extent of hybridization. In central Alberta, Canada, two economically and ecologically important pine species, lodgepole pine and jack pine, have a distributional overlap. They are closely related species, and when they hybridize they produce viable offspring. Reliably distinguishing hybrid stands from pure stands has not been possible using conventional morphological and chemical analyses therefore we employed a panel of microsatellites as a more accurate means of identification. Analysis of over 2000 trees using two different Bayesian assignment methods (STRUCTURE and NEWHYBRIDS) has allowed us to reliably identify hybrids, and redefine the extent of the hybrid zone, and the parental distributions. We have found that the parental ranges cover a larger geographic extent than what was previously thought, and as a result, the hybrid zone covers a larger region as well. This information has been used to document the host-range expansion of mountain pine beetle and will be useful in the future for modelling mountain pine beetle epidemics.

RAD Sequencing: A Method for Population Genomics

John W. Davey, Simon W. Baxter, Chris D. Jiggins & Mark L. Blaxter

University of Edinburgh, UK

Next generation sequencing technologies are making a substantial impact on many areas of biology. However, genomic-scale population genetics studies, particularly from organisms with previously unsequenced genomes, remain prohibitively expensive. Restriction-site associated DNA sequencing, or RAD sequencing, is a high-throughput method that samples genomes at reduced complexity across target individuals. It promises to deliver high resolution population genetic data – thousands of sequenced markers across many individuals – for any organism at reasonable costs. I will demonstrate the potential of RAD Sequencing by presenting the creation of high-density linkage maps of all 31 chromosomes of the diamondback moth *Plutella xylostella*, using only a single lane of Illumina sequencing and no reference genomic information.

Molecular and morphological variation within the sentinel species, *Lumbricus rubellus*

Robert K Donnelly, Michael W Bruford, Jake G Bundy, A John Morgan & Gabriela A Pinto-Juma

University of Glamorgan, UK

Mitochondrial sequence analysis has revealed the presence of two distinct genetic lineages within the earthworm species *Lumbricus rubellus*. The existence of these two lineages could complicate ecotoxicological studies which apply the species as a sentinel of soil contamination as the two lineages may respond differently to contamination. Analysis of *L. rubellus* and three congeneric species revealed a degree of sequence divergence between the lineages of *L. rubellus* that was comparable to that between different species in the Lumbricus genus. This divergence was investigated further by sequencing the repeat and flanking regions of eight microsatellites. This revealed no evidence of inter-lineage hybridisation, with the discovery of substantial differentiation between lineages within the normally highly-conserved microsatellite flanking regions. Analysis of a novel morphological trait located on the anterior segments was investigated for inter-lineage identification and a blind-trial indicates the utility of this trait to differentiate between the two lineages.

Molecular evolution of a Y chromosome to autosome gene duplication in *Drosophila*

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In contrast to the rest of the genome, the Y chromosome is restricted to males and lacks recombination. As a result, Y chromosomes are unable to respond efficiently to selection, and newly formed Y chromosomes degenerate until few genes remain. The rapid loss of genes from newly formed Y chromosomes has been well-studied, but gene loss from highly degenerate Y chromosomes has only recently received attention. Here, we identify and characterize a Y to autosome duplication of the male fertility gene kl-5, which occurred during the evolution of the testacea group species of *Drosophila*. The duplication was likely DNA-based, as other Y-linked genes remain on the Y-chromosome, the locations of introns are conserved, and expression analyses suggest that regulatory elements remain linked. Genetic mapping reveals that the autosomal copy of kl-5 resides on the dot chromosome, a tiny autosome with strongly suppressed recombination. Molecular evolutionary analyses show that autosomal copies of kl-5 have reduced polymorphism and little recombination. Importantly, the rate of protein evolution of kl-5 has increased significantly in lineages where it is on the dot vs. Y-linked. Further analyses suggest this pattern is a consequence of relaxed purifying selection, rather than adaptive evolution. Thus, while the initial fixation of the kl-5 duplication may have been advantageous, slightly deleterious mutations have accumulated in the dot-linked copies of kl-5 faster than in the Y-linked copies. Because the dot chromosome contains seven times more genes than the Y, and is exposed to selection in both males and females, these results suggest that the dot suffers the deleterious effects of genetic linkage to more selective targets compared to the Y-chromosome. Thus, a highly degenerate Y chromosome may not be the worst environment in the genome, as is generally thought, but may in fact be protected from the accumulation of deleterious mutations relative to other nonrecombining regions that contain more genes.

Next generation sequencing in non-model organisms: A case study of the Ruff (*Philomachus pugnax*)

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The sequencing revolution of the last five years has opened up enormous possibilities for molecular ecologists to apply genomics tools to their favourite study organisms, even in the absence of previous genetic data. However, the analysis of such data is non-trivial and many analytical methods are still in their infancy. I will discuss some important general points to consider when a non-model species “goes genomic”. I will also highlight some of the possibilities and pitfalls of the new technologies, using next generation transcriptomic data from the Ruff (*Philomachus pugnax*) as an example. By sequencing the transcriptome (all expressed genes) of a non-model organism, it is possible to get data on both sequence variation and gene expression levels (a method known as RNA-Seq). We have used this approach to investigate differences in plumage coloration and mating strategies in this lekking bird species. Ruff males show enormous variation in the coloration of ornamental feathers. This colour polymorphism is also linked to reproductive strategies with dark males defending territories on the leks, while white morphs function as satellites without establishing territories of their own. Previous work has shown that the male coloration has a very strong genetic component but the exact genes involved have not been identified. By using next generation sequencing data we now try to pinpoint the genetic regions determining these ecologically important traits.

Concordance between species trees and gene genealogies with multiple mergers

Bjarki Eldon & James Degnan

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Concordance between species trees and gene genealogies are considered for gene genealogies allowing multiple mergers of ancestral lineages. Donnelly and Kurtz, Pitman, and Sagitov independently introduced coalescent processes (Lambda coalescent) that allow asynchronous multiple mergers of ancestral lineages. Kingman's coalescent allows only two ancestral lineages to merge at a time. Lambda coalescents may be more appropriate than Kingman's coalescent for some marine organisms with high fecundity and broadcast spawning. Multiple mergers, ie allowing any number of ancestral lineages present each time to coalesce, complicates computations. Two methods will be presented to compute the concordance, one relies on enumeration of all possible sequences of mergers, and the other is the spectral decomposition of the rate matrix. Results will be presented for two and three species and small sample sizes from each, for different Lambda coalescents.

Does it matter where we publish?

Adam Eyre-Walker & Nina Stoletzki

University of Sussex, UK

Most scientists spend considerable amount of time and energy trying to get their work published in the most prestigious journals. But does publishing in certain journals ultimately affect the impact of the science? Will a paper published in Genetics, ultimately have as much impact as a paper of similar quality published in Nature? We have recently attempted to answer this question by comparing the number of citations gained by papers that are judged to be of similar quality between journals. We find that articles published in more prestigious journals do obtain more citations, even when we control for the quality of the science.

DNA double-strand break repair and the evolution of intron density

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The density of introns is both an important feature of genome architecture and a highly variable trait across eukaryotes. This heterogeneity has posed an evolutionary puzzle for the last 30 years. Recent evidence is consistent with novel introns being the outcome of the error-prone repair of DNA double-stranded breaks (DSBs) via non-homologous end joining (NHEJ). Here we suggest that deletion of pre-existing introns could occur via the same pathway. We propose a novel framework in which species-specific differences in the activity of NHEJ and homologous recombination (HR) during the repair of DSBs underlie changes in intron density.

Population structure in a migratory freshwater fish of the genus Prochilodus

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Federal University of Pará, Brazil

Prochilodus nigricans is a detritivorous, migratory fish species widely distributed in the Amazon Basin. In order to study genetic variation and structuring in this species, we sequenced and analysed a 502 base-pair fragment of the mitochondrial D-loop region of 104 specimens caught in 6 localities along the river Tapajós, one of the largest Amazon tributaries. Sequences were aligned to other congeneric species and had their phylogenetic relationships estimated with Maximum Parsimony, Maximum Likelihood and Bayesian methods. Diversity indexes, neutrality tests, demographic parameters, and genealogical analyses were used to assess population structuring and demographic events shaping the genetic variation. Both phylogenetic and population genetic analyses show that populations from the middle and upper course of the Tapajós differ significantly from those from the lower course. Evidence from population analyses also demonstrate structuring between middle and upper course populations. Migration estimates and diversity indexes suggest that populations from the headwaters of the river act as the main source of diversity, acting as a source population to the middle course population. Contrary to findings in related species of Prochilodus, and migratory fish in general, *Prochilodus nigricans* populations are highly structured in the study area.

Adaptation to drought in two wild tomato species: the evolution of the *Asr* gene family

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University of Munich, Germany

Wild tomato species are a valuable system to study local adaptation to drought: they grow in diverse environments ranging from mesic to extremely arid conditions. We investigated the members of the *Asr* gene family, which are reported to be involved in water stress response. We analyzed the evolution of the *Asr* gene family in populations of two closely related species, *Solanum chilense* and *S. peruvianum*. We applied a candidate gene approach to investigate the evolutionary forces acting at the *Asr* genes. Strong purifying selection has been acting at *Asr1* and in contrast to previous reports we did not detect evidence for positive selection at *Asr2*. *Asr4* shows patterns of local adaptation in a *S. chilense* population that lives in an extremely dry environment. We discovered a new member of the gene family, *Asr5*. Our results show that the *Asr* genes constitute a dynamic gene family. We describe an excellent example for tandem arrayed genes which are of importance in adaptation. Taken the potential distribution of the species into account, it seems that *S. peruvianum* can cope with a great variety of environmental conditions, whereas *S. chilense* seems to be undergoing local adaptations more frequently.

Combining markers into haplotype can improve population structure inference

Lucie Gattepaille

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Since the recent development of high through-put genotyping methods, the density of available sets of genetic markers has markedly increased. Because of the dense sets of markers, linkage disequilibrium starts to play a major role for the studies of population structure or for the studies of assigning individuals to groups. We investigate the effects of combining markers into haplotype-loci on population structure analyses and assignment problems. We introduce a new statistic derived from information theory, the Gain of Informativeness for Assignment (GIA) from haplotype data, a quantity that measures the differential of the information for assigning individuals to populations using haplotype data compared to using two loci separately. We show on simulation studies that the accuracy of the assignment of individuals to populations can be improved by combining markers into haplotypes using GIA. We thus provide an original method for dealing with sets of markers in high LD.

Dynamics of diversification by coevolution: the case of the self-incompatibility locus

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Self-incompatibility (SI) enables hermaphrodite plants to avoid self-fertilization and mating with close relatives. It is based on recognition and rejection of pollen by pistils if they express cognate specificities at two linked genes, one expressed in pollen and one in pistils. While these genes are typically highly multiallelic, the conditions allowing the emergence of new SI haplotypes remain mysterious. Indeed, the evolution of new SI haplotypes entails tight coevolution between the two genes, since any mutation affecting one of the two genes only would result in a non-functional self-compatible haplotype. We first document the combinations of selfing and inbreeding depression where diversification at the S-locus is deterministically expected to occur by investigating analytically the fate of mutations in an infinite population. We then use simulations to show that the conditions allowing diversification are far less stringent infinite populations with recurrent mutations, suggesting that diversification in a panmictic population is indeed a likely phenomenon for diversification in SI species. Interestingly, we found that the rate of diversification is not expected to be time-linear, new SI haplotypes emerging more readily in populations with a low number of extent SI haplotypes.

Quantifying the variation in the effective population size within a genome.

Toni I. Gossmann & Adam Eyre-Walker

University of Sussex, UK

The genetic variation of a population, the so called effective population size (*Ne*), is one of the most fundamental parameters in population genetics. It is thought to vary across the genome as a consequence of differences in the rate of recombination and density of selected sites; this is most vividly illustrated by the strong correlation between the level of nucleotide diversity and the rate of recombination in Drosophila species. Although it is known that there is intragenomic variation in the effective population size, little is known about how much variation in the effective population size there is and if the amount of variation differs between organisms. Here, we have used a hierarchical Bayesian analysis to quantify the amount of variation in the effective population size across a genome from levels of nucleotide diversity and divergence at putatively neutral sites. We have applied our methodology to data from 10 species including *Drosophila melanogaster*, humans, mouse, yeast and many plants. We show that the variation is relatively modest in most of the investigated species.

Determinants of Synonymous and Nonsynonymous Variability in Three Species of *Drosophila*

Penelope R. Haddrill, Kai Zeng & Brian Charlesworth

University of Edinburgh, UK

We estimated the intensity of selection on preferred codons in *Drosophila pseudoobscura* and *D. miranda* at X-linked and autosomal loci, using a published dataset of 67 loci, and an improved method that accounts for demographic effects. We found evidence for stronger selection at X-linked loci, consistent with their higher levels of codon usage bias. The strength of selection and mutational bias in favour of unpreferred codons were similar to those found in other species, after taking into account evidence for a recent expansion in population size in *D. pseudoobscura*. We examined correlates of synonymous and nonsynonymous diversity in these species, and found no evidence for effects of recurrent selective sweeps on nonsynonymous mutations, probably because this set of genes have much higher than average levels of selective constraints. Subsequent analysis of a published dataset on *D. melanogaster* provided evidence for the effects of selective sweeps of nonsynonymous mutations on linked synonymous diversity, but only in the subset of loci that experienced the highest rates of nonsynonymous substitutions, and not at more slowly evolving loci. Our correlational analysis of this dataset suggested that both selective constraints on protein sequences and recurrent selective sweeps affect the overall level of codon usage.

Evolutionarily labile social organisation in an ant

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The degree to which complex traits are evolutionarily labile is an important question in evolutionary biology. We have studied among population variation in a complex trait - the level of reproductive sharing among cohabiting queens (reproductive skew). Genetic evidence shows that social organisation in multiple queen nests of the widespread ant *L. acervorum* varies strikingly among populations. In most populations multiple queens reproduce in each colony, leading to low relatedness among colony members (polygyny) but in populations from Spain only one queen reproduces so multiple queen nests have high relatedness (functionally monogynous). Further evidence shows functional monogyny in Japanese populations. Phylogenetic analysis of mtDNA rejects the hypothesis that functionally monogynous populations (Spain and Japan) are monophyletic, so populations with different social organisations are not cryptic species. These data suggest that the degree of reproductive skew amongst queens in *L. acervorum* is a labile trait. We discuss how selection might drive the evolution of alternative social organisations and the relevance of these findings to the assumptions of models of reproductive skew that rely on social contracts.

Recombination and the Undesirable Hitchhiker

Matthew Hartfield & Sarah P. Otto

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When new advantageous alleles arise and spread within a population, deleterious alleles at neighbouring loci can hitchhike alongside them. If recombination is low enough, these deleterious hitchhikers can spread to fixation within the population, introducing a fixed mutation load. We use branching processes and diffusion equations to calculate the probability that a deleterious allele hitchhikes and fixes alongside an advantageous mutant, as a function of the recombination rate between the two loci and the strength of selection acting on each allele. As expected, the probability of fixation of a deleterious hitchhiker rises with the selective advantage of the sweeping allele and declines with the selective disadvantage of the deleterious hitchhiker. The region of parameter space within which deleterious alleles are likely to hitchhike to fixation is smaller than that for neutral alleles, because recombinant chromosomes that free the advantageous allele from the deleterious allele are favoured whenever they appear. We consider these results in light of human genetic data to infer how likely it is that such deleterious hitchhikers have occurred in our recent evolutionary past.

Human impacted landscapes facilitate hybridization between a native and an introduced tree

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Hybridization between native and introduced species is a conservation concern as well as a potential source of adaptive variation, but the spatial and temporal dynamics of this process, particularly for long lived species, remain elusive. The temperate forest tree *Juglans ailantifolia* (Japanese walnut) was introduced to North America in the mid nineteenth century, where naturalized populations coexist with the native tree *Juglans cinerea* (butternut). We used microsatellite and chloroplast markers to characterize the influence of anthropogenic landscapes on the extent, direction, and spatial distribution of hybridization at 137 locations across the majority of the range of the native species. Admixture (at nuclear markers) across all anthropogenic sites reached nearly 70%, while fragmented and continuous forests showed minimal admixture (7.5 and 2.5%, respectively). In addition, anthropogenic sites exhibited higher inheritance of the introduced chloroplast (95%) than the forested sites (59 and 69%). Our results show a strong influence of habitat on the introgression process, and we suggest that even small forested habitats have served as a partial barrier to hybridization, a key consideration for conservation planning. We suggest that similar levels of hybridization may occur across the range of other North American forest trees.

Detecting hybridization between willow grouse (*Lagopus lagopus*) and rock ptarmigan (*L. muta*) in Central Sweden through Bayesian admixture analyses and mtDNA screening

Jacob Höglund, Marıa Quintela & Carl-Gustaf Thulin

Uppsala University, Sweden

To assess whether any genetic exchange is occurring among Willow grouse (*L. lagopus*) and rock ptarmigan (*L. muta*), we used different Bayesian-based admixture analyses of multilocus genotypes determined at twelve microsatellite loci. We also obtained mitochondrial COI-sequences from a selected number of individuals to infer the maternal geneflow and potential introgression. The capacity of our panel of microsatellite markers to detect hybridization was verified using assignments of simulated genotypes. We then evaluated the extent of hybridization in an actual sample of 111 individuals collected in a 100-km2 area in the Scandinavian mountain range. An admixed condition was verified in a suspected hybrid, that seemed to carry a *L. muta* genotype with partial *L. lagopus* introgression. In addition, more than 4% of *L. lagopus* showed signs of hybridization under the most conservative scenario with respect to discrepancies between population assignment methods. This was unexpected, given that no *L. lagopus* displayed any apparent intermediate plumage features. Furthermore, interspecific geneflow of mtDNA haplotypes was lower than expected. Hybridisation may be expected to increase if the climate gets warmer as the habitat overlap between the species will become more extensive. We discuss whether hybridisation is a threat to the long-term survival of any of the two species.

Predictions of Native American population structure using language covariates in a hidden regression framework

Flora Jay, Olivier François & Michael Blum

University of Grenoble, France

We investigate to which extent geography and languages can predict the genetic structure of Native American populations. Our approach is based on a Bayesian latent cluster regression model in which cluster membership is explained by geographic and linguistic covariates. After correcting for geographic effects, we find that the inclusion of linguistic information improves the prediction of individual membership to genetic clusters. We further compare the predictive power of Greenberg's and The Ethnologue classifications of Amerindian languages. We report that The Ethnologue classification provides a better genetic proxy than Greenberg's classification at the stock and at the group levels. Although high predictive values can be achieved from The Ethnologue classification, we nevertheless emphasize that Choco, Chibchan and Tupi families do not exhibit a univocal correspondence with genetic clusters.

Searching for consistent signals of balancing selection in *Plasmodium falciparum* genes.

Daniel Jeffares, Catherine Ingle, Magda Sekowska, Leonardo Basco, David Conway, Sanjeev Krishna, Abdoulaye Djimdé, Mike Quail, Quan Long, John Welch & Manolis Dermitzakis.

University College London, UK

Study of genetic diversity, population structure and selection in the malaria parasite *Plasmodium falciparum* are motivated both by academic interest, and by the importance of these factors for achieving economically feasible control of these parasites by antimalarial drugs and vaccines. To this end we sequenced 94 genes (chosen from various biologically interesting groups) from 84 malaria infected blood samples, from four locations (the Gambia, Cameroon, Mali and Thailand). Most (75%) of these samples contain multiple *P. falciparum* genotypes, with what look to representing complex within-mosquito and within-human populations. Comparing our biologically signifcant genes groups to a set of 25 randomly selected genes, we use various orthologonal methods to look for consistent signals of balancing selection (which may be indicative selection to avoid host defenses). We find signals consistent with balancing selection in some expected groups such as known antigen genes (from Mu et al 2007) and Surfins (which are present on the surface of infected red blood cells), but not in others such as Rhoptry neck proteins (localized to the organelles facilitate parasite invasion of red blood cells).

The potential for intralocus sexually antagonistic polymorphism among genomic regions

Crispin Y. Jordan & Deborah Charlesworth

University of British Colombia, Canada; University of Edinburgh, UK

Intra-locus sexually-antagonistic polymorphism (SA) occurs when one allele is advantageous in one sex (say, males) but deleterious in the other (females), and a second allele has the opposite qualitative fitness effects. SA causes high fitness variation in some populations, and can affect the evolution of sexually dimorphic and sexually-selected traits. Also, when an SA locus lies in a recombining region of newly-evolved sex chromosomes (a pseudo-autosomal region, "PAR"), selection can favour reduced recombination between the SA locus and a sex-determining region, which can lead to the evolution of heteromorphic sex chromosomes. Despite its importance in these processes, theory has produced conflicting predictions for the prevalence of SA polymorphism among genomic regions (autosomes, non-recombining regions of sex chromosomes, PAR), depending on the strength of selection and assumptions regarding dominance. We provide the most comprehensive analysis to date that accounts for these assumptions, and conclude that the PAR always has the greatest potential to harbour SA polymorphism. Autosomes also have high potential for SA polymorphism, particularly when alleles are (at least) partly dominant in the sex in which they are favoured.

Experimental evolution of temperature adaptation in *Drosophila simulans*

Martin Kapun, Viola Nolte, Robert Kofler, Pablo Orozco, Thomas Flatt & Christian Schlötterer

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Drosophila simulans originated in Madagascar, colonized Africa and recently spread around the world. The colonization of new habitats and climate zones might thus have involved multiple adaptations to new environmental conditions. Various genome scans aiming to identify the underlying adaptations faced the problem to disentangle demography and selection. Here, we use a complementary approach to understand thermal adaptation in *D. simulans* by experimental evolution selecting to segregating variation in a natural outbred population from Northern Portugal. A starter-population of *D. simulans* was split into two subsets of five replicate populations each, which are maintained at two different temperatures extremes (10°C and 28°C respectively). Using pooled samples from individuals from different generations, we trace adaptation on the genomic scale by 2nd generation sequencing (Illumina GA IIx).

Recombination in the extinction/recolonisation model

Jerome Kelleher, Nick Barton & Alison Etheridge

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The extinction/recolonisation model solves several major problems associated with the classical models of diffusive gene flow in a spatial continuum. In this model, random events kill some fraction of the population in a particular region, which is then repopulated by the offspring of some small number of parents drawn from nearby. We show how recombination can be incorporated into this model by considering two different approaches: recombination between events and recombination within events.

Gene flow constrains adaptive divergence between trout populations

Irene Keller, Jolanda Schuler & Ole Seehausen

Eawag (Swiss Federal Institute of Aquatic Science and Technology), Switzerland

The European trout (*Salmo trutta* species complex) is widely distributed in Switzerland across a broad altitudinal range from lowland rivers to alpine streams. Historically, the major European river systems contained different, evolutionarily distinct trout lineages, and some genetic differentiation has persisted in spite of human-mediated dispersal through stocking. We used AFLP-based genome scans to investigate the extent of potentially adaptive divergence between major drainages and across altitudinal gradients replicated in different rivers. At some markers, band frequency was repeatedly associated with altitude. Overall, however, the extent of potentially adaptive divergence was larger between drainages than across altitudinal transects. Within rivers, the number of markers showing evidence of divergent selection between population pairs increased with geographical but not altitudinal distance between sites. Together, these results suggest a constraining role of gene flow on the extent of potentially adaptive divergence between Alpine trout populations.

Genetic basis of the Gouldian finch (*Erythrura gouldiae*) colour polymorphism

Kang-Wook Kim, Sarah Pryke, Simon Griffith & Terry Burke

University of Sheffield, UK

The Gouldian finch (*Erythrura gouldiae*) has three genetically determined colour morphs in the wild: red, black and yellow. The inheritance pattern of the colour polymorphism in this species is known to be under the control of two Mendelian loci. Previous studies have shown assortative mating and genetic incompatibility among the morphs in a captive population and it is possible that these morphs represent incipient species. However, as yet we do not know the molecular genetic basis of the polymorphism. In this project, genetic differentiation between black and red morphs in the wild population was studied to examine the incipient species hypothesis. By constructing a genetic map of the Gouldian finch and linkage mapping of the Red colour gene in informative crosses, the location of the locus that controls this polymorphism was identified. In this talk I will discuss how assortative mating based on genetic polymorphism may shape the genome of the Gouldian finch and how the structure of the genome may influence the observed genetic incompatibility. Dense marker development by RAD sequencing and intensive sequencing using a sequence capture array are in progress to identify the colour polymorphism gene and causative mutation.

Positive and negative selection on non-coding DNA upstream and downstream of protein-coding genes in wild house mice

Athanasios Kousathanas, Fiona Oliver, Daniel L. Halligan & Peter D. Keightley

University of Edinburgh, UK

Studies of adaptive evolution of non-coding DNA using variations of the McDonald-Kreitman test have been conducted so far only in Drosophila and humans. These studies suggest that the fraction of substitutions that have been driven to fixation by positive selection (α) is high in non-coding DNA of Drosophila (~40-60%) and close to zero in humans. We have studied selection in non-coding regions upstream and downstream of protein-coding genes in the house mouse *Mus musculus castaneus*, by analyzing polymorphism data for 78 loci from 15 wild-caught *M. m. castaneus* individuals and divergence to a closely related species, *Mus famulus*. Using the polymorphism data, we estimated the distribution of fitness effects of new mutations, and inferred that most new mutations in upstream and downstream regions behave as effectively neutral (~70%) and that only a small fraction (~10-20%) are strongly negatively selected. We estimated α to be significantly lower (~10%) for upstream and downstream regions than for non-synonymous sites (~50%). However, we also found that the ratio of adaptive to neutral divergence (ωα) is very similar for non-synonymous sites and upstream and downstream regions (~5-10%). Our results indicate that upstream and downstream regions in *M. m. castaneus* experience similar absolute rates of adaptive substitution to non-synonymous sites, but they differ in the rate of nearly neutral mutation.

RAD Genotyping Facilitates Rapid Marker Discovery in Species Without a Reference Genome

Maureen Liu

University of Nottingham, UK

With recent advances in sequencing technologies, there has been a rapid growth in the number of genomes sequenced. However, limited by factors such as read-length and assembly, many species of interest in the fields of evolution and ecology still lack a reference genome, and are not benefiting from current ultrahigh-throughput sequencing techniques. Here we show how a Solexa-sequencing based technique (Restriction-site associated DNA (RAD) markers, Johnson et al 2008) has enabled us to rapidly identify genetic markers associated with a Mendelian trait, the maternal effect chirality locus, in a non-model organism, *Lymnaea stagnalis*. These markers will provide good candidates for future fine mapping

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Persistence of polymorphism in MHC Class II of guppy (*Poecilia reticulata*) may not rely on parasite mediated selection only.

Violaine Llaurens, Mark McMullan & Cock van Oosterhout

University of Hull, UK

MHC polymorphism has been proposed to be due to balancing selection exerted through host-parasite coevolution. This parasite mediated selection particularly targets the peptide-binding region of MHC (PBR), which is involved in the specific recognition of parasites. Here we investigated how the sequence polymorphism of MHC class IIB genes of the guppy *Poecilia reticulata* is maintained. Four populations of guppies were sampled in Trinidad (N= 79), and 1068 bp sequences of MHC class II gene covering Exon 2, Intron 2 and Exon 3 were amplified and sequenced. Consistent with the prediction of host-parasite co-evolution, a significant diversification signal was detected in the PBR (Tajima's D = 2.34, $P < 0.05$). Although intron sequences exhibit a high diversity, 27 exon 2 sequences shared the same intron 2 sequence. Within this cluster of sequences, the signal of diversifying selection on the PBR was not detected (D = -1.54, $P > 0.05$). Since this absence of signal was not due to small sample size, we hypothesize that this large amount of diversity not maintained by parasite mediated selection might be due to a larger effective size for these sequences, resulting from gene conversion among different MHC loci.

Evolution of hypervariability in phospholipase A2 toxins from snake venoms

Anita Malhotra, Simon Creer, Karen Dawson & Roger S. Thorpe

Bangor University, UK

Snake venom toxins are good candidates for studying the acquisition of novel functions though gene duplication and nucleotide subsitution. Phospholipase A2 (PLA2) enzymes are a major component of viperid snakes and have been relatively well studied at the protein level. However, evolutionary analysis of these toxins has been hampered by lack of power due to poor sampling, unavailability of a robust species phylogeny, preponderance of cDNA sequences, and computational limitations. Here, we report on a new analysis of over 100 new full-length gene sequences obtained from 20 Asian pitviper species. After detection and removal of PCR artefacts and recombinants, and compensating for heterotachy, we reconstructed the history of duplication and loss by reconciliation with a recently published, well-resolved, multilocus species tree for pitvipers. Inferences possible include: a minimum of least 6-9 gene copies per genome, high rates of gene turnover, and a strong signal of lineage-specific and site-specific selection (both positive and purifying) in protein-coding regions. In contrast to previous analyses we find that duplication events are concentrated at the tips of the tree, suggesting that major functions such as presynaptic neurotoxicity have been evolved convergently multiple times in the evolutionary history of vipers.

Sex ratio fluctuations favour the evolution of sex-changing strategies

Stefano Mariani, Julien Chopelet & Robin Waples

University College Dublin, Ireland

Population genetics theory predicts that skewed sex ratios will reduce the effective population size (*Ne*). Sex-changing species exhibit skewed sex ratios, thus leading to the expectation of lower Ne compared to gonochorists. However, *Ne* also greatly depends on the variance in individual lifetime reproductive success (*Vk*), which must be taken into account when comparing sex-changers with gonochorists. Here, we test whether sequential hermaphrodites have lower Ne than gonochorists, by modifying previous life-history models to fit for species with two sexes, with and without sex-change. We estimated *Vk*, *Ne* and generation time when individuals are stratified according to their age, sex and age-at-sex-change. We modelled these key parameters under contrasting scenarios in which different sets of demographic parameters generate different degrees of size advantage, which to date remains the most robust mechanism to explain the selective advantage of sex-change. Interestingly, while no significant differences between sex-changers and gonochorists were observed under weak size advantage, sequential hermaphrodites were found to exhibit higher Ne than gonochorists in a strong size advantage scenario, provided that sex ratios are equally biased. This finding suggests that sex-change might be an advantageous strategy to compensate for skewed sex ratios, thereby circumventing the risks associated with reduced Ne.

Unraveling patterns of genetic diversity in a salmonid metapopulation

Alexia Massa-Gallucci, Martin O'Grady & Stefano Mariani

University College Dublin, Ireland

Brown trout (*Salmo trutta L.*) is a highly polytypic and ecologically diverse species, of traditionally high economic and societal value. In Ireland, in particular, brown trout is one of the most popular species for sport fisheries and as such supports an important tourist industry. Lough Mask and its inflowing streams, situated in the west of the country, are one of the largest and most important wild salmonid catchment in Ireland. Over the years, Lough Mask has gained an international reputation as an excellent salmonid fishery, in particular for wild brown trout and the long-lived, highly-prized, piscivorous "Ferox" eco-phenotype, which appears to be reproductively isolated from sympatric brown trout. Such biodiversity is not only threatened by fisheries, but also by a variety of anthropogenic drivers that may alter the demographic and ecological equilibria of these populations, with the consequent loss of diversity and unique adaptive potential. The present study unravels the patterns of neutral genetic diversity in the Mask catchments, identifying the most divergent populations and streams, and estimating the proportional contributions of the different spawning components to the lake stock. We delineate complex metapopulation structure, with varying degrees of population divergence among streams, from extreme isolation (FST>0.1) to complete homogeneity. The information obtained is expected to play a vital role in the long term conservation of trout fisheries in Ireland.

Multiple evolutions of alternative reproductive modes in tadpole shrimps

Thomas C. Mathers, Robert L. Hammond, Ronald A. Jenner, Bernd Hanfling, Thorid Zierold, and Africa Gomez

University of Hull, UK

The Notostraca, or tadpole shrimps, are an ancient order of branchiopod crustaceans whose morphology has remained stable for millions of years. In contrast to this morphological stasis reproductive modality within the order is highly variable with three systems found: gonochorism, the presence of separate males and females in a 50:50 ratio; obligatory selfing hermaphroditism, where females have evolved ovotestis and make up 100% of the population; and androdioecy, where males and selfing hermaphrodites coexist. It is assumed that gonochorism is the ancestral reproductive mode of the order and that from this androdioecy and selfing hermaphroditism have evolved. To test this assumption and to investigate the flexibility of reproductive mode evolution within the order we constructed, for the first time, a resolved notostracan phylogeny based on a supermatrix alignment of three mitochondrial and four nuclear genes. Using this tree an ancestral character state analysis based on parsimony was conducted. This approach confirmed gonochorism as the ancestral state in tadpole shrimps and that from this alternative reproductive modes have evolved independently on at least four occasions. Moreover, the rare reproductive mode androdioecy, which is documented in only a handful of animal species, has evolved on at least three occasions.

The Role of Pathogens in Ageing

C. D. McClure, W. Zhong & N. K. Priest

University of Bath, UK

Pathogens are a major burden to many organisms in the natural world. They have therefore likely played a major role in shaping patterns of senescence, the increase in risk of death with age. However, the relationship between pathogenic immunity and age-related mortality is largely unknown. Here we report a study in which 10,000 fruit flies, *Drosophila melanogaster*, were exposed to live spores of the fungus, *Metharhizium robertsii*, and the resulting patterns of senescence were studied under different fungal growth rate conditions. The results indicate that the growth rate of the pathogen can have profound consequences for the death rate of the host. We argue that host-pathogen interactions may be critical for our understanding of the evolution of ageing.

Spatial and temporal variation at the Major Histocompatibility Complex (MHC) in Trinidadian guppy populations

Mark McMullan, Joanne Cable & Cock van Oosterhout

University of Hull, UK

The MHC has become a paradigm to study sexual and natural selection. Variation at the MHC is often higher than can be explained by neutral evolution, and selection by a diverse parasite fauna is thought to maintain the high level of polymorphism. The Red Queen hypothesis proposes that parasites adapt to escape recognition by MHC molecules, which invokes counter-adaptations in the MHC. This can maintain a high MHC diversity and increases the rate of adaptive evolution. Here I present an analysis on the temporal variation in MHC IIB diversity in guppies (*Poecilia reticulata*) of Trinidad. MHC alleles are rapidly replaced over time by alternative alleles, which is consistent with the Red Queen hypothesis. However, alternative explanations are possible, and I use computer simulations to explore those. I show that balancing selection increases the turnover rate of alleles, and that this rate is accelerated by a: high level of genetic polymorphism in the metapopulation, high migration rate, small effective population size, and large population size fluctuations. This study shows that rapid changes in MHC alleles should not necessarily be taken as evidence of Red Queen dynamics through host-parasite co-evolution and that host-demography can significantly affect temporal genetic changes at the MHC.

It's a kind of magic: Ecological speciation in *Heliconius* butterflies

Richard M. Merrill & Chris D. Jiggins

University of Cambridge, UK

Traits under disruptive ecological selection that also promote assortative mating can facilitate speciation in the face of gene flow. However, the existence of such 'magic traits' in nature has been considered unlikely. Mimicry in tropical butterflies has long been championed as an example of adaption driving speciation. In the Neotropical genus *Heliconius* pairs of unpalatable species converge on the same bright warning-pattern to more efficiently advertise their distastefulness to predators. Closely related taxa often belong to different mimicry rings, and experiments have shown that males use colour pattern during mate recognition. Hybrids display intermediate warning patterns that are unlikely to be recognized as distasteful. The sister species, *Heliconius melpomene* and *H. cydno* are sympatric across much of Central and northern South America. Using model butterflies we reveal selection against non-mimetic hybrid colour patterns between these two species. In addition, by testing mate preferences in hybrid males we demonstrate a genetic association between male mate preference and wing colour pattern. In particular, male preference for red patterns is associated with the locus responsible for the red forewing band. Thus we demonstrate disruptive selection acting on a mating trait that is genetically associated with the corresponding mate preference.

Comparative analysis of teleost fish genomes reveals novel patterns of intron size distribution

Steve Moss, Dave Lunt & Domino Joyce

University of Hull, UK

Here we present a comparative genomics analysis of introns using five teleost fish. This was undertaken using a novel software pipeline, alongside established bioinformatics tools. Although there are many similarities in intron size and frequency, both between these fish and with regards to other vertebrates, the comparisons show unique features, especially with regard to the zebrafish *Danio rerio*. Our analyses demonstrate a displacement in the distribution of large intron size classes in *Danio*, with a greater frequency of large introns compared to other fish. Analysis of repeat elements between fish genomes indicates that these likely contribute significantly to total genome size variation. Although within introns we find a diversity of repeat types these cannot account for the observed size differences for which it seems a different mechanism is responsible.

Species delimitation using AFLPs: A comparative methodological assessment

Mrinalini, Roger S. Thorpe, Simon Creer & Anita Malhotra

Bangor University, UK

The determination of species boundaries in morphologically undifferentiated populations is forming an increasingly important area of research. While a majority of studies often rely on phylogenetic analysis of mitochondrial and/or nuclear gene sequences to resolve cryptic species, AFLPs have often proved to be useful by providing a substantial amount of genome-wide information essential for establishing the degree of reproductive isolation between populations. However, the effectiveness of various analysis methods used to analyze AFLP datasets for differentiation of cryptic species is still unclear and several new methods have been recently proposed. We conducted a comparative study of some of the widely used and latest analysis methodologies used for inferring population structure. The genus *Cryptelytrops*, a group of venomous pitvipers from South-East Asia, was used for this study as the species of this and other South-East Asian pitviper genera are morphologically conservative and have proved difficult to classify in the past. The results show that while AFLP is undoubtedly a useful tool for cryptic species recognition, the use of multiple types of analysis is critical for making robust inferences of populations structure.

Pattern of chicken domestication and dispersion in the Old World: A Bayesian perspective

Mwacharo J.M., Quentin A. & Hanotte O.

University of Nottingham, UK

Genetic evidences show that domestic chicken are derived from multiple maternal origins in Asia. The timing of domestication and dispersion of the species across the world has been subject to debate. Similarly, the timing of expansion of the species as main agricultural commodity is poorly documented. We investigated these questions through Bayesian analysis, using the BEAST software (Drummond and Rambaut, 2007), of the first hypervariable region (incorporating the first 397 base pairs) of mitochondrial DNA D-loop sequenced in over 5000 African and Asian village chicken. Our findings indicate that the relative time to the most recent common ancestor (TMRCA) for different mitochondrial DNA haplogroups differ significantly across the modern day geographic range of the wild ancestor. Also, our results support different arrival time of the species in different geographic areas outside the geographic range of the wild progenitor species. Bayesian skyline plots for different geographic regions reveals that chicken became an important livestock species at different time periods in Asia and Africa. It seems that domestic chicken took time to be adopted as a livestock species in different geographic regions within Asia and Africa in spite of being currently the most widely distributed domestic animal species across the globe.

Parasites in ecological speciation; heritability of parasite resistance in the three-spined stickleback

Aliya El Nagar, Job de Roij & Andrew MacColl

University of Nottingham, UK

The role of parasites as potential drivers in ecological speciation has been studied less than other ecological causes of divergent selection. In order to understand whether parasites contribute towards ecological speciation, it must initially be ascertained whether they can influence the diversification of populations. Populations of the three-spined stickleback *Gasterosteus aculeatus* are highly diverse in the wild, and carry different species and abundances of parasites. Infection experiments on progeny of various populations has shown that resistance to parasites is genetically determined because when treated equally and exposed to the same parasite strains, resistance differed. The next step is to understand how the resistance trait is genetically determined. This can help when searching for genes involved in resistance. Investigating how the quantitative trait works can also show how hydridization between populations influences fitness, and whether this in turn could create a breeding barrier. Line cross analysis between a resistant and susceptible population was conducted. Parentals, F1, F2, and back-crosses were bred and infected with a digenean trematode *Diplostomum pseudospathaecum*. Preliminary results show how the resistance trait may be genetically controlled.

Cryptic diversity of endemic Indirana frogs of the Western Ghats biodiversity hotspot

Abhilash Nair, Sujith V. Gopalan, Sanil George, K. Santhosh Kumar, Amber G. F. Teacher & Juha Merilä

University of Helsiniki, Finland

Recent studies have shown that the number of amphibian species in biodiversity hotspots may be heavily underestimated, and many new species are constantly being reported from these hotspots. For successful conservation and management strategies to be implemented within these hotspots, better understanding of the species diversity and their evolutionary relationships is required. Frogs of the genus *Indirana* belong to the endemic family Ranixalidae, and are found exclusively in the Western Ghats biodiversity hotspot, in southern India. We used three mitochondrial (16S, 12S and CO1), and two nuclear (rag1 and rhodopsin) gene fragments to investigate the genetic diversity within the endemic *Indirana* genus, using Bayesian, maximum likelihood and maximum parsimony methods. The results suggest that the species diversity within the *Indirana* is much higher than previously anticipated. Instead of the previously expected six species within this region, the analyses identified eleven clades with high levels of sequence divergence (3.6 – 22.2%). Hence, each of these clades is likely to represent a distinct species. In general, the results suggest the existence of multiple unrecognised cryptic lineages within *Indirana*, which are likely to have narrower distribution ranges and lower abundance than the taxonomic units into which they are currently assigned.

The effect of gene-flow at a secondary contact zone on hybrid morphology in the cichlid fish *Astatotilapia calliptera*

Paul Nichols, Cock van Oosterhout & Domino Joyce

University of Hull, UK

In theory, hybridization between divergent lineages that have been isolated for prolonged periods of time can generate phenotypic novelty that may drive adaptive radiation. Here, we document the phylogeographic history of allopatric populations of *Astatotilapia calliptera*, the only member of the Lake Malawi haplochromine cichlid radiation to be found both within and outside Lake Malawi. Mitochondrial DNA haplotypes of *Astatotilapia spp*. approximately 4 million years divergent have colonised Lake Malawi and we present evidence of a secondary contact zone in the southern region of the Lake Malawi catchment. Having used RFLPs to distinguish between the haplogroups where they occur in sympatry, we used microsatellite analysis to demonstrate gene flow between them, both in the wild and in the lab, where pre-mating behavioural barriers were examined in mate-choice experiments. Having demonstrated that hybridization at this zone of contact is feasible, F2 hybrids were reared in the laboratory in order to quantify phenotypic variance compared to F2 purebred lines, with the expectation that an increase in phenotypic variation is consistent with the hypothesis that hybridisation could have lead to the generation of phenotypic novelty in the Lake Malawi species flock. The results of this morphological analysis are presented.

Characterising genetic diversity in the world of next generation sequencing

Richard Nichols & Bob Verity

Queen Mary, University of London, UK

We will soon be able to obtain whole-genome sequences from multiple individuals from several populations of the same species. Rather than simply cataloguing this variation, we argue that it will be useful to characterise it in terms of simple genetic models with a few parameters. In the past, with data from fewer loci, this task has been done using the trusty workhorse of the *Fst* statistic, and we propose that this approach will continue to be effective in many cases. We show how the underlying logic can be extended to models with more biologically meaningful parameters. In some cases they allow estimates of migration or population size, which will be of interest in themselves; in other cases these models will enable us to identify outlying loci of particular interest - and to better identify the results of processes such as hybridisation, admixture and introgression.

Higher-than-expected genetic diversity and potential genetic adaptability in the reef coral *Pocillopora damicornis* at a high latitude region.

A. M. E. Noreen, M. J. H. van Oppen, S. Schmidt-Roach & P. L. Harrison

National U. of Singapore

Theory predicts that small, peripheral, and geographically isolated populations are more likely to have detrimental genetic factors that increase extinction risk. However, if remote populations persist, there may arise unique, locally adapted, evolutionary significant genotypes. Subtropical reefs in Eastern Australia are an ideal location to test these predictions due to their small population sizes, marginal habitat, and distance from the Great Barrier Reef (~400-1000 km). Using a slowly-evolving mitochondrial marker as well as microsatellites, we investigated genetic diversity at, and estimated ecological and evolutionary connectivity between, reefs and coral communities of subtropical Eastern Australia and the Great Barrier Reef in the model coral *Pocillopora damicornis*. Ecologically relevant gene flow was rare, with pairwise F_{ST} values significant for all but two location pairs. Evolutionarily significant gene flow was complex, with evidence of both genetic isolation and genetic connectivity at some locations. The highest-latitude coastal and offshore populations were each dominated by a different, unique mitochondrial haplotype, indicating local adaptation, or maintenance of ancestral haplotypes. However, the microsatellite data supported a low, non-zero level of genetic connectivity, potentially contributing genetic diversity and benefiting peripheral populations' long-term persistence. Additionally, there was no significant difference detected in allelic richness over the >1,200 km sampling range. Thus, given the higher-than-expected mitochondrial and microsatellite genetic diversity present in range edge *P. damicornis* populations, their adaptive potential may be higher then previously hypothesized. However, the apparent complexity of *P. damicornis* evolutionary history at several subtropical locations warrants further investigation.

The maintenance of sex - was Fisher right?

Len Nunney

University of California, Riverside, USA

A recurring theme of the early 1900s was that sexual reproduction was maintained because, although it conferred no immediate benefit to individuals, it conferred a species-level evolutionary advantage. This view of the long-term advantage of sexual reproduction over asexual alternative (formalized by Fisher and others) has been supported by the phylogenetic distribution of parthenogenetic species within clades: their closest relatives are usually sexual species, but opposed by the long-term persistence of some asexual lineages. However, the view that sex could be maintained solely by its long-term benefit fell apart following Maynard Smith's 1971 demonstration of the 2-fold per generation fitness cost of sex. The recognition of this cost of sex (or William's cost of meiosis) has prompted 40 years of research into whether short-term benefits of sex can overcome its disadvantage. Establishing such high short-term benefits has proved elusive, and maybe it is time to reconsider a lineage selection model for the maintenance of sex where no such advantage is necessary.

Correlations between heterozygosity and reproductive success in the blue tit (*Cyanistes caeruleus*)

Juanita Olano-Marin, Jakob C. Mueller & Bart Kempenaers

Max Planck Institute for Ornithology, Germany

Correlations between marker heterozygosity and variation in fitness-related traits, known as heterozygosity-fitness correlations (HFC), have been widely studied in natural populations. However, the biological causes underlying the HFC are still not clearly understood. We provide evidence for a positive effect of individual multilocus heterozygosity (MLH) on the annual reproductive output of male and female blue tits from an Austrian population. We genotyped the breeding individuals with a panel of 79 microsatellite markers. These markers had a known location in a passerine genome and were classified either as potentially functional or neutral. The effects of MLH and the strength of heterozygosity-heterozygosity correlations (HHCs) were generally stronger for "neutral" loci. We document the occurrence of some consanguineous matings and found evidence for a cryptic genetic population structure, supporting a role of inbreeding in the observed HFC. We argue that "neutral" markers are better predictors of inbreeding and that the characteristics of the loci used in HFC studies should be taken into account when interpreting the results.

Genomewide signatures of adaptation in *Drosophila melanogaster*

Pablo Orozco-terWengel, Martin Kapun, Robert Kofler, Ram V. Pandey, Viola Nolte & Christian Schlötterer

VetMedUni Vienna, Austria

An open question in evolutionary biology is how species adapt to new environments, and whether this process occurs via the change of single genes or large networks of interacting genes. Replicate cultures in laboratory experimental evolution experiments in combination with the latest sequencing technologies provide the unique opportunity to study these questions on a genomic scale with a single base pair resolution. By introducing a natural *D. melanogaster* population from Northern Portugal to a novel laboratory environment, we studied the contribution of standing variation to adaptation. We identified selected variants by a consistent change in allele frequency in three replicate populations propagated in the novel environment. We show that already after 15 generations numerous loci showed a significant and consistent change in allele frequencies across the replicate populations. Although selected genes are found on all chromosomes, we see an excess of those in the right arm of the 3rd chromosome, suggesting an influence of the inversion 3R Payne.

Using phylogeography to prioritise conservation effort in the giant otter

Rob Pickles, Bill Jordan & Jim Groombridge

Institute of Zoology, London, UK

The giant otter is an endangered mustelid found throughout north and central South America. We aimed to resolve the phylogeographic structure of the species to pinpoint important centres of genetic diversity. We used DNA extracted from a combination of spraints collected in the field and museum samples to achieve complete coverage of the giant otter's range. Sequence data of 950 base pairs of the Mitochondrial genome comprising Cytochrome B and the Control Region were used to resolve phylogeographic structure. This was complemented by genotyping individuals from 4 populations using 13 microsatellite loci and comparing allele frequencies. Sequence data revealed a moderate level of genetic diversity in the species as a whole and subdivision into four distinct mitochondrial lineages. Population structure was confirmed by allele frequencies, which revealed the Orinoco and north-west Amazonian populations to be partially admixed whereas the Bolivian Amazon population displays a degree of reproductive isolation in both the mitochondrial and nuclear genomes to suggest warranting the term Evolutionary Significant Unit.

Drift widens the expected cline but narrows the expected cline width

Jitka Polechová & Nick Barton

Institute of Science and Technology, Austria

Random genetic drift shifts clines from side to side, alters their width, and distorts their shape. The wobbling in position makes the expected cline wider. However, locally, drift drives alleles towards fixation, so individual clines can often be narrower. The relation between the deterministic cline width, expected cline width, and width of the expected cline is driven by the average standardized variance

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Age of the extant human malaria parasite *Plasmodium vivax*

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National Institute of Malaria Research, India

Plasmodium vivax is the most prevalent human malaria parasite that diverges from monkey malaria parasites via host switch. Age of *P. vivax* was addressed mainly using mitochondrial genome diversity, however so for no nuclear markers have been identified which showed a comparable level of evolutionary history. Here we are addressing age of *P. vivax* using selectively neutral putative housekeeping genes (nuclear) and proposed to be good genetic marker for the understanding of demographic events and evolutionary history of an organism. We have identified ten putative housekeeping genes, and were amplified and sequenced from 100 *P. vivax* Indian field isolates. DNA sequence analysis for SNPs variation in the ten housekeeping genes revealed substantial number of SNPs (75) in coding and intronic regions. The coalescence analysis of the TMRCA (Time to the Most Recent Common Ancestor) estimate of the age of extant *P. vivax* revealed 232,000-304,000 years that suggest for an ancient evolutionary history of this parasite. This age estimate is very close to the age previously identified using mitochondrial genome diversity and is consistent with the hypothesis that extant *P. vivax* was parasite of hominoid before it became human parasite.

The role of compensatory mutation in the evolution of gene regulatory networks

Nicholas K. Priest

University of Bath, UK

The fate of a deleterious mutation depends, in part, on its mutational context. A mutation that would otherwise be deleterious can compensate when it restores the function of a previously non-functional genetic pathway. Compensatory mutations have been largely ignored because they are thought to be rare. As a consequence, we do not understand their basic properties. Are they generally of large or small effect? Where in the gene pathway are compensatory mutations likely to occur? What is the rate of compensatory mutation? Here, we address these questions using a common paradigm in evolutionary systems biology, the gene regulatory network. Similar to previous approaches, we examined the consequences of mutation on the stability of thousands of randomly sampled gene regulatory networks; but, we did not disallow the possibility that some mutations – deleterious on the own – may have compensatory effects. The talk will discuss our findings.

Patterns of codon usage bias in *Silene latifolia*

Suo Qiu, Roberta Bergero, Kai Zeng & Deborah Charlesworth

University of Edinburgh, UK

Patterns of codon usage bias (CUB) convey useful information about the selection on synonymous codons, and can also be informative about the distinctive evolutionary properties of sex chromosomes. Here, we study CUB in *Silene latifolia*, a species of interest for studying the early stages of sex chromosome evolution. We have obtained >1608 EST fragments by 454 sequencing. Using three different methods, we conservatively define 21 preferred codons. Interestingly, the preferred codons in *S. latifolia* are almost identical to those in Arabidopsis thaliana, despite their long divergence time. For the 43 genes with both exon and intron sequences, we find a positive correlation between gene expression and GC content at third codon positions, but a strong negative correlation between expression and intron GC content, suggesting that the CUB in *S. latifolia* is more likely to be due to natural selection than to mutational bias. An analysis of 10 sex-linked genes reveals that the X chromosome has experienced more unpreferred to preferred than preferred to unpreferred substitutions, suggesting that it may be evolving higher CUB. In contrast, numbers of substitutions between preferred and unpreferred codons are similar in both directions in the Y-linked genes, contrary to the expectation of genetic degeneration.

Analysis of a model introduced by Kimura.

Gael Raoul

University of Cambridge, UK

In 1965, Kimura introduced a very simple integro-differential model to describe the evolution of a population structured by a phenotypic trait. Numerically, this model seems to capture important phenomena of evolution: speciation, branching, etc... However, apart from numerics, it seems very difficult to use this model to get a simplified view of evolutionary properties of a population. On the contrary, Adaptive Dynamics is a (relatively) simple tool, that describes the evolution of simplified (monomorphic) populations. We were able to establish links between the model introduced by Kimura and Adaptive Dynamics, in particular conserning evolutionarily stable populations. The model of Kimura then allow us to investigate the phenotypic diversity within a given species.

Applications of genetical genomics

Kermit Ritland, Jasmine Ono & Rockney Albouyeh

University of British Columbia, Canada

Gene expression can be regarded as a quantitative trait, subject to all the forces of inheritance and evolution of all other phenotypic traits. In modern genomics, there are several advances for evaluating gene expression at levels, which I will not mention. My main point will be that gene expression differences can be layered on top of pedigree or population relatedness, giving two major avenues of investigation and insight. (1) Within populations, segregating pedigrees allow networks of gene interaction and central "master" genes to be inferred, and heritability of gene expression to be quantified. (2) Among populations (or species), expression differences reveal forces of natural selection (drift vs. diversifying vs. stabilizing selection). In both cases, examples from spruce and poplar are given.

Mitochondrial DNA differentiation within the Eastern Kalahari Bushveld lineage of *Micaelamys namaquensis* (Rodentia: Muridae)

Isa-Rita M Russo, Christian T Chimimba & Paulette Bloomer

Univeristy of Pretoria, South Africa & Cardiff University, UK

The Namaqua rock mouse *Micaelamys namaquensis* Smith, 1834, is distributed in southern Africa and is restricted to rocky outcrops or boulder-strewn hillsides. We conducted a phylogeographic analysis among 10 localities of the Eastern Kalahari Bushveld lineage of *M. namaquensis* based on mitochondrial DNA cytochrome b sequences. A pattern of phylogenetic continuity with a lack of spatial separation was observed. Despite the restricted number of samples for some localities demographic analysis suggests that the lineage has expanded and that this expansion may have followed environmental changes associated with natural habitat modification in the recent past. Dispersal is greatly influenced by landscape heterogeneity, resource distribution and population densities and in turn determines the genetic structure of populations. The estimates of historical female gene flow resulting from the present study suggest reasonable levels of connectivity among localities although some areas appeared to act as sinks and others as sources. The description of the genetic structure within this lineage is fundamental to understanding its evolutionary history and will assist in future efforts to conserve overlooked small mammal biodiversity in South Africa.

Characterisation of the transcriptome of a wild bird, the great tit (*Parus major*), using next generation sequencing

Anna W. Santure, Jake Gratten, Jim A. Mossman, Ben C. Sheldon & Jon Slate

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Great tits are a model wild study system in evolutionary biology, and their long term study has enabled the examination of areas as diverse as the evolution of life history traits in response to climate change and the heritability of personality. However, identifying the genomic regions underlying these traits has been restricted by a lack of genetic resources. Great tits have been monitored in Wytham Woods since the 1940s, with extensive morphological, life history and pedigree information and blood samples available, providing tremendous opportunity to integrate the findings of previous quantitative genetic studies with genomic approaches to locate the regions of the genome contributing to variation in these traits. Here, we outline the sequencing, de novo assembly and analysis of transcripts pooled from ten wild great tit fledglings. Approximately 1.4 billion bases of DNA were generated and assembled into 95,979 contigs, one third of which aligned with known zebra finch and chicken genes. Over 35,000 single nucleotide polymorphisms were identified, which, along with the transcriptome sequence, provide a valuable toolkit for QTL mapping and association studies in this population, and highlight the power and speed at which next generation sequencing enables the generation of sequence data in a wild species.

The contrasting roles of seed and pollen migration in niche evolution.

Frank Shaw, Ruth G Shaw, Ophelie Ronce & François Rousset

Hamline University, USA

We examine through simulation the demographic and evolutionary dynamics of a two-patch metapopulation. One population, initially at mutation-stabilizing selection-drift equilibrium in its patch, disperses seeds and pollen into a second patch where the optimum differs enough so that most migrants are too maladapted to survive. Holt and others (2003) found that after an exponentially distributed waiting period, the second population leaps rapidly to carrying capacity. We expand on their results, finding that the waiting time depends on number of loci affecting the trait, mutation rate and variance, and migration rate of both seeds and pollen. In particular, pollen flow consistently inhibits the adaptation of the second population to its patch optimum.

Population genetics and phylogeography of the long-snouted seahorse *Hippocampus guttulatus*: The use of genetic tools in marine conservation

Paul Shaw & Heather Koldewey

University of Stirling, UK

Seahorses are unique fishes, with extraordinary and well-known biological and ecological traits: male seahorses become ‘pregnant’, carrying the embryos until giving birth to live young. Seahorses are site faithful once recruited to a site, and are generally monogamous. Research has mainly centred on these aspects of unusual biology, and only recently has the genetics of these curious fishes been studied. Previous genetic work on seahorses has mainly concentrated on taxonomic identification and phylogenetics. The study presented here is the first to investigate population genetics of the European long-snouted seahorse, *Hippocampus guttulatus*. The study compares population structuring using mitochondrial DNA (control region and cytochrome b gene) sequences and microsatellite loci. Results are discussed comparing levels of gene flow and patterns of genetic differentiation across the northeastern Atlantic Ocean, Mediterranean Sea and Black Sea. Furthermore potential mechanisms and barriers to gene flow are examined. Finally, some conservation and management suggestions for *H. guttulatus* are made.

The distribution of genetic effects on fitness

Ruth Shaw, Frank Shaw & Charles Geyer

University of Minnesota, USA

The genetic variation for fitness in a natural population, which represents its capacity to adapt to prevailing conditions, is often considered to be small, as expected for populations that have been subject to the same selection regime long enough to reach equilibrium. However, particularly with increasing attention to rapid environmental change, it is questionable whether populations are at evolutionary equilibria. Consequently, genetic variation for fitness may be considerable in nature. In addition to the difficulty of acquiring the data needed to evaluate Vg for fitness, statistical challenges have obviated direct evaluation of the distribution of genetic effects on fitness. I have taken advantage of recently developed aster modeling of fitness to obtain estimates of this distribution for several plant populations growing in nature and will present these findings.

Single introduction of topmouth gudgeon into Europe from an admixed source population followed by long-distance dispersal

Andrea Simon, Cock van Oosterhout & Bernd Haenfling

University of Hull, UK

The topmouth gudgeon (*Pseudorasbora parva*), an Asian cyprinid was introduced into Europe in the 1960s and it is now found in at least 32 countries outside its native range. A 700 base pair fragment of the mitochondrial cytochrome b gene was analysed to examine different models of colonisation and spread within the invasive range and to investigate possible contributing factors to the species' invasion success. Haplotype and nucleotide diversity of the introduced populations from continental Europe was higher than that of the native populations, apart from two recently introduced populations from Britain, which showed low levels of variability. Based on coalescent theory, all introduced and some native populations showed a relative excess of nucleotide diversity compared to haplotype diversity. This suggests that these populations are not in mutation-drift equilibrium, but rather that the relative inflated level of nucleotide diversity is consistent with recent admixture. This study elucidates the colonisation patterns of *P. parva* in Europe and provides an evolutionary framework of their invasion. It supports the hypothesis that their European colonisation was initiated by their introduction to a single location or small geographic area with subsequent long distance dispersal. Furthermore, it was preceded by, or associated with, the admixture of genetically diverse source populations that may have augmented its invasive-potential.

No evidence for a bottleneck of modern human origins in Africa

Per Sjödin, Mattias Jakobsson & Michael Blum

University of Uppsala, Sweden

We investigate the hypothesis that the human species suffered from a severe population size reduction 130 thousand years ago at the end of the penultimate glacial period. Using 61 genetic markers from three African populations we conclude, utilizing an ABC approach, that there is no genetic evidence to support such a bottleneck scenario.

Using a multi locus approach to infer the phylogeography of *Drosophila mojavensis*

Gilbert Smith, Konrad Lohse, William J. Etges, & Michael G. Ritchie,

University of St Andrews, UK

Phylogeography aims to examine historical or contemporary structure between populations and closely related species. Traditional methods of phylogenetic inference use many individuals and few loci, often only mtDNA. However there is evidence that using more loci rather than increasing within-population sampling could improve parameter estimation. We have used this sampling strategy to examine divergent populations of a cactophilic fly, *Drosophila mojavensis*. This species is distributed across several geographically distinct regions in NW Mexico and Southern California, using different host cacti to carry out its life cycle in these areas. Genetic analyses have shown transgressive genetic variation exists for adaptations to host cactus use, so it is of interest to examine the divergence of these populations in order to understand the historical population structure and gene flow between them. Previous work has revealed conflicting results in this system, so we aimed to obtain an estimate of the demographic parameters associated with each population divergence event. We amplified 15 intronic regions of the X chromosome and compared these sequences to previously published autosomal data. We performed coalescent simulations in the program IMa2 to estimate divergence times, population sizes and migration events. Our results are consistent with recent diversification with little on-going gene flow between these populations.

Patterns of MHC diversity in the early stages of divergence: insights from an endemic island bird

Lewis G. Spurgin, Juan Carlos Illera & David S. Richardson

University of East Anglia, UK

Major histocompatibility complex (MHC) genes are essential components of the vertebrate immune system, encoding for molecules that bind to pathogenic peptides, thereby triggering an immune response. MHC genes have attracted a lot of attention from evolutionary biologists, mainly due to their remarkable levels of allelic variation and nucleotide diversity, which are thought to be generated and maintained by pathogen-mediated balancing selection. We have used next-generation sequencing technology to assess patterns of population-level MHC diversity in the bird Berthelot's pipit (*Anthus berthelotii*), across the North Atlantic islands of Macaronesia. Previous work has shown that this species has recently colonised Macaronesia, and that little gene flow occurs between populations, providing an ideal opportunity to study how MHC genes operate in the early stages of divergence. We use a clustering approach alongside recent advances in codon-based models of detecting selection to examine how different MHC lineages have diverged across populations, as well as the role of selection in shaping these patterns of divergence.

The evolution of PRDM9 binding motifs in humans

Nina Stoletzki

Harvard Medical School - Brigham & Women's Hospital, USA

The PRDM9 protein has recently been shown to play a major role in determining recombination hotspot distribution in the human genome.

Genetic variation and evolution of the PRDM9 has hence attracted much interest. PRDM9 is a zinc finger protein that trimethylates lysine 4 of histone 3. The gene and particularly its sites involved in DNA binding appear to evolve rapidly across diverse metazoan taxa. Several human PRDM9 alleles have been identified. However, the evolution of the DNA sequence to which PRDM9 binds - and whether it is under selection - is unclear. There may be positive selection that creates or destroys binding sites, or purifying selection that maintains them.

The predicted recognition motif of PRDM9 in the DNA fits to a previously identified 13-mer motif that is associated to 40% of human recombination hotspots. To test for selection, I use the motif logo to assign functionally more and less important motif sites for which I then compare polymorphism and divergence data. The process of recombination itself will destroy the initiating motif, and the effect of gene conversion has been demonstrated for the human PRDM9 motif. To not confuse selection with gene conversion, I consider the latter and its bias towards GC.

Neutral (SNP) vs. adaptive (MHC) genetic diversity in black grouse populations of various degrees of isolation.

Tanja Strand, Segelbacher G, Quintela M, Xiao L, Axelsson T, Jansman HAH & Höglund J.

Uppsala University, Sweden

In the past neutral markers have mainly been used in studies of genetic variation in threatened populations. However, markers from selected genes have increasingly come in to use especially when the evolutionary and adaptive potential of a population is under focus. One way to study adaptive genetic diversity in wild birds is to use a so called "Bottom-up" approach and use candidate genes such as MHC. The black grouse is a widely distributed bird species in Eurasia with both highly threatened (red listed) populations and large, healthy populations were hunting is permitted. We have studied 14 contemporary and historic European black grouse populations. The contemporary populations were divided into three different categories; 1) continuous, 2) isolated, and 3) small and isolated, respectively. We have screened black grouse at MHC class II B loci using RSCA genotyping. We have also typed the populations for variation at ten microsatellite loci and 34 SNP (Single Nucleotide Polymorphisms) loci. We asked if the MHC diversity deviated from the genetic diversity derived from microsatellites and SNPs, and such patterns differs among markers and in populations of various sizes and degree of isolation. Preliminary analyses suggest that for all classes of markers, the number of polymorphic loci is highest in the continuous populations and historic central European populations, and lower in the two isolated categories. Observed heterozygosity was highest in the continuous populations. One isolated population show signs of retained genetic diversity and also low *Fst* when compared with the continuous populations. The continuous black grouse population in the Alps showed high *Fst* when compared to the other populations. This last result may be explained by the fact that although Alpine black grouse populations are in connectivity, the Alps is surrounded by poor black grouse habitat and may have been isolated from the rest of the distribution for longer times. In summary, the patterns observed in this study suggest that genetic drift in small and isolated populations is the major force shaping the genetic diversity of the isolated European black grouse populations regardless of choice of marker.

Transcriptome analyses reveal that worker behaviour in a eusocial wasp originates by delaying social maturation

Seirian Sumner, Solenn Patalano, Pedro Ferreira & Roderic Guigo

Institute of Zoology, London, UK

Social animals achieve highly complex societies via a division of labour, whereby individuals may specialise in different behaviours. The eusocial insects (termites, ants, some bees and wasps) epitomise this in the form of reproductive (queen) and non-reproductive (worker) castes, who may differ in behaviour, morphology, fertility and physiology. The altruistic behaviour of workers in eusocial insects was 'potentially fatal' for Darwin's theory of natural selection, and the mechanisms underlying the origins of worker behaviour remain unclear today. Using 454 technology, we sequenced the transcriptomes of four behavioural phenotypes of the primitively eusocial wasp *Polistes candensis* to compare genome-wide differences in transcription. We found large differences in the numbers of genes and functional groups expressed by queens and workers. Our results suggest that worker behaviour evolves through transcriptomic 'shut-down' of socially dominant traits, such that workers are delayed reproductives who express a small subset of the transcriptional activity found in queens. This simple 'Russian doll' model for the origins of worker behaviour suggests that the same mechanism may underlie the evolution of worker behaviour in eusocial insects and helpers-at-the-nest in cooperative breeding vertebrates.

The Evolutionary Consequences of Male-killing: Sex and Ladybirds!

Tamsin Majerus

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Male-killing endosymbionts have been widely reported in the invertebrates and are highly prevalent in the Coccinellidae. The presence of male-killers can lead to extreme bias in host population sex ratios and may have important and far-reaching consequences for the life-history and evolution of their hosts. Male-killers may have direct and indirect effects on host fitness and reproductive behaviour, as well as affecting the host genome, either via strong selection pressure imposed by highly female-biased population sex ratios or by selective sweeps caused as a male-killer conferring an advantage to infected individuals spreads through a population. Maternal inheritance of two phenotypic indicators, low egg hatch rate and female-biased progenic sex ratio, are used to identify females harbouring male-killers. Antibiotic treatment is used to elicit a cure and confirm the bacterial nature of the agent. PCR assays and sequencing have then been used to identify the bacteria responsible. Generally these have proved to be reliable tools in a variety of insect species in orders including Coccinellidae, Lepidoptera and Diptera. However, following the identification of male-killing suppressors, where the phenotypic expression of male-killing shows evidence of interaction with host factors, a more stringent combination of phenotypic and molecular methods is required.

Genetic Differentiation of the Twin Spotted Wainscot Moth (*Archanara geminipuncta*) in UK *Phragmites* reedbeds

Alison Thomas, Victoria Hartley, Philip Pugh & Deborah Clements

Anglia Ruskin University, UK

The stem boring activities of the larvae of the twin spotted wainscot moth (*Archanara geminipuncta*) have significant influence on the ecology of UK *Phragmites* reed beds. Severe caterpillar infestation can, for example, prevent flowering with inevitable consequences for associated seed feeding bird species. On the otherhand, larvae and pupae form an important food source for breeding birds. The DNA profiling technique (ISSR-PCR) has been used to assess genetic variability within and between four central UK populations of this keystone species. As individuals were collected their location was recorded using GIS providing a unique record of the genetic spatial distribution within each reed-bed habitat. The binary (presence/absence of amplified bands) data matrices constructed from the ISSR-PCR profiles were analysed in MVSP via principal components analysis (PCA), which applied Kaiser's rule. This showed strong genetic differentiation of *A geminipuncta* populations between habitats. This was confirmed by application ofGenAlEx software (6.3) to the data which produced a PhiPT value of 0.598 ($p < 0.001$). These findings have high relevance for the management of reed beds, which are becoming increasingly fragmented, and their associated fauna communities. Partitioning of genetic variation between populations and increasing isolation are early stages in an extinction vortex.

The Global Invasion of the Harlequin Ladybird (*Harmonia axyridis*)

Cathleen E. Thomas, Eric Lombaert, Remy Ware, Renate Zindel, Alexandre Aebi, Arnaud Estoup & Lori Lawson Handley

University of Hull, UK

Species invasions have wide ranging ecological and economical impacts, and are one of the greatest threats to biodiversity, agriculture and human health. Despite this, there is still much we do not understand with regard to why only certain species become successful invaders, what determines their success and what impacts they have on other species. The successful invasion of different continents by *Harmonia axyridis* (harlequin ladybird) provides a unique opportunity to investigate the invasion history of a highly invasive species, and to attempt to identify common factors underlying invasion success. Molecular genetic data can provide vital insights into invasion dynamics. We have used mitochondrial DNA sequence data to investigate the global invasion of *H. axyridis*, as part of an ongoing study. By analysing individuals from native and invasive populations we aim to understand: (1) the source(s) and routes of spread of the invasion and (2) the genetic characteristics of the founding population(s). The findings of this study complement microsatellite data being gathered on the same harlequin populations, as well as data on the presence of bacterial endosymbionts carried by individuals within these populations. This will provide a powerful dataset, making this one of the best case studies for understanding species invasions.

Why species have an edge

John R.G. Turner & H. Yan Wong

University of Leeds, UK

Why do species not expand their ranges continuously and indefinitely? Perhaps the necessary mutations cannot occur where they are needed, and are not adaptive where they occur. Simulations have been performed on a metapopulation spatial lattice with "minimum contact", with the species able to produce mutations which adapt it to a continuous environmental gradient. Within the dynamic edge of the species, these range extending mutations can prevail only if they have a middling phenotype: adapting to a moderate change in the environment. Mutations producing large extensions of range, and those producing only small extensions, are "sieved" out, and are relatively unsuccessful. This restricts the rate of evolution, but predicts that species should nonetheless expand steadily at a moderate pace. That they seem not to, therefore, has to be explained by a. the exhaustion of the mutational repertoire, and/or b. competitor species. This second explanation suggests some interesting questions about the maintenance of the planetary biodiversity gradient.

On the fixation process of a beneficial mutation in a variable environment

Hildegard Uecker & Joachim Hermisson

University of Vienna, Austria

For adaptive evolution to proceed, it is not sufficient that new beneficial mutations enter a population, they also must survive genetic drift, get established and finally rise to fixation. Ecological changes often happen at the time scale of this fixation process, affecting the population size and the selective advantage of the mutation. We consider the fixation process of a beneficial allele in a variable environment, allowing for explicit time-dependence of the population size $N = N(t)$ and the selection coefficient $s = s(t)$. Using the theory of inhomogeneous branching processes, we derive analytical approximations for the fixation probability and the distribution of passage times for the beneficial allele to reach a given intermediate frequency.

Genetic stock structure as a base for management: The case of turbot.

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ILVO-Institute for Agricultural and Fisheries Research, Belgium

Many commercial fish stocks have severely declined over the past decades. This raises the question whether current management strategies are sufficient to guarantee the sustainable exploitation of marine resources. A key to sustainable management is matching biologically relevant processes to management activities. Novel insights into the genetic structure and the identification of fish populations should contribute to our understanding of the demography and connectivity of fish stocks to be implemented in management actions. Our research focuses on turbot (*Scophalmus maximus L.*), a valuable commercial species living in the northeast Atlantic Ocean, the Mediterranean Sea and the Black Sea. In 2004, the European Community asked the International Council for the Exploration of the Sea (ICES) for management advice. Our unique research aims to identify the true population structure, to assess the spatial and temporal stability of sub-populations, and to determine the environmental factors influencing the observed spatial structuring of genetic diversity. We have analyzed the samples of turbot on a pan-European scale (Atlantic and Mediterranean basins) using genetic fingerprints of eighteen microsatellite markers. We can refute the hypothesis that turbot is a panmictic marine species, with clear basin-wide separations and more subtle differentiation patterns on a smaller geographical scale. We plan further comparative population genetic analyses, by integrating our results with the genetic patterns of other flatfish, to help improve the sustainable management of mixed stock fisheries.

Selection and population differentiation for song and cuticular hydrocarbons in *Drosophila montana*

Paris Veltsos, Claude Wicker-Thomas, Roger K Butlin & Michael G. Ritchie

University of St Andrews, UK

We have analysed variation in two important traits for sexual selection: courtship song and cuticular hydrocarbons (CHCs) between two populations of Drosophila montana. The two populations represent distinct phylogeographic clades which have probably evolved separately for ca. 0.5 MY. We examined the relationship between these traits and reproductive success within populations. The traits were scored from wild-collected isofemale lines, and their offspring, from three generations raised in the lab. Results: Courtship traits differed between the two populations. Both courtship song and CHCs predicted mating success but strongest sexual selection was exerted on song parameters. The relationship between traits and mating success did not differ strongly between populations for song, while for CHCs there were differences related to sexual dimorphism. Discussion: Sexual selection was strong on traits in which the two populations have diverged. With the exception of song interpulse interval (IPI), quadratic effects did not significantly influence mating success. Net selection acted on more limited characters than total selection, suggesting that variation in some characters is counteracted by variation in others. The potential of environmental selection in influencing traits under sexual selection is also discussed.

A Modern Perspective on Measures of Population Differentiation

Robert Verity & Richard Nichols

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We will soon be able to obtain whole-genome sequences from multiple individuals from several populations of the same species. Rather than simply cataloguing this variation within and among individuals, we argue that it will be useful to characterise it in terms of simple genetic models with a few parameters. In the past, with data from fewer loci, this task has been done using the trusty workhorse of the *Fst* statistic, however, recent work has called into question the validity of using *Fst* as a single sufficient statistic to describe structure. We show how the logic of *Fst* can be extended, in some cases estimates of migration or population size will be of interest in themselves, in other cases the models will enable us to identify outlying loci of particular interest - and to better identify the results of processes such as hybridisation, admixture and introgression.

Estimating selfing rates from multilocus genotype data

Jinliang Wang, Kermit Ritland & Y. A. El-Kassaby

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Several methods have been developed to estimate the selfing rate of a population from a sample of individual genotypes at a number of marker loci. These include the homozygosity excess (F_{IS}) method, identity disequilibrium (ID) method, progeny array (PA) method and individual assignment (InStruct) method which assigns individuals into populations and estimates the selfing rate of each population. Overall, PA is the best method because it is accurate and robust to the violations of many assumptions (e.g. perfect genotype data without misscoring, random biparental mating, and inbreeding equilibrium), and also because it can estimate other interesting properties of a mixed mating system such as the “correlation of paternity” and “correlation of selfing”. In practice, however, it is often difficult to obtain progeny arrays, especially for animal species. In this paper, we propose a method to reconstruct the pedigree of a sample of individuals taken from a monoecious diploid population under the mixed (selfing-outcrossing) mating system, using the multilocus genotypes of sampled individuals. An individual is from selfing and outcrossing if its two inferred parents are the same individual and distinctive individuals, respectively. Selfing rate is thus estimated by the frequency of selfing progeny in the sample. The method enjoys the many advantages of the PA method without the need of knowing the relationships among sampled individuals, although such information, if available, can be utilized to help the inference. Furthermore, the new method accommodates genotyping errors, estimates allele frequencies jointly, and is robust to non-random biparental mating and other assumptions which are critical to other methods. Both simulated and empirical data were comparatively analysed by different methods to investigate the accuracies and statistical properties of the methods.

The relative roles of demic diffusion and local recruitment in the spread of horse domestication

Vera Warmuth, Anders Eriksson, Mim Bower, Graeme Barker & Andrea Manica,

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The origin and geographic spread of horse domestication is controversial and poorly understood. One of the greatest gaps in our knowledge concerns the extent to which domestic horses were moved out of the area of their initial domestication in the western Eurasian steppe. In this paper, we investigate this question by developing a spatially explicit framework to fit genetic data from more than 300 horses, sampled throughout northern Eurasia and genotyped at 26 autosomal microsatellites. We first reconstruct the history of the wild ancestor of domestic horses, and find strong support for an expansion out of East Asia around 150kya. Next, we reconstruct the geographic spread of domestication out of the western steppes 6kya, allowing for both movement of domesticated animals and recruitment from local wild populations. Our results strongly suggest that the spread of horse domestication across the steppes involved both a movement of domestic horses out of western Asia and a continuous recruitment of local wild stock, thus consolidating seemingly contradictory evidence from Y chromosomal and mitochondrial DNA.

Human genes have not reached their full regulatory potential

Maria Warnefors & Adam Eyre-Walker

University of Sussex, UK

Human gene expression is governed by an intricate combination of transcription factors, miRNAs, splicing factors and other regulators. Genes cannot support infinitely complex regulation, due to sequence constraints and the increased likelihood of harmful errors. However, the upper limit of regulatory complexity in the human genome is not known. Here we provide evidence that human genes are currently not operating at their maximum capacity in terms of gene regulation. We analyse genes spanning the full spectrum of eukaryote evolution, from primate-specific genes to genes present in the eukaryote ancestor, and show that older genes tend to be bound by more transcription factors, have more conserved upstream sequences, generate more alternative isoforms, house more miRNA targets and are more likely to be affected by nonsense-mediated decay and RNA editing. These results cannot be explained by overrepresentation of certain functional categories among younger or older genes. Furthermore, the increase in complexity is continuous over evolutionary time, without any signs of saturation, leading to the conclusion that human genes have the capacity to evolve even more complex gene regulation in the future.

Dynamics of adaptation in large sexual populations

Daniel Weissman & Nick Barton

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In a large population, multiple beneficial mutations may arise simultaneously. In order for them all to fix, they must occur in the same individual or be brought together by recombination. This requirement sets an upper limit to the rate of adaptation. We find the scaling of the rate of adaptation with population size, mutation rate, strength of selection, and recombination rate in a toy model of adaptation.

Discovering hidden biodiversity - population genetics of cryptic *Gammarus fossarum* species

Anja Marie Westram, Irene Keller, Caroline Baumgartner & Jukka Jokela

EAWAG (Swiss Federal Institute of Aquatic Science and Technology), Switzerland

Biodiversity is not always visible at first glance. Morphological similarity can hide huge genetic diversity - to be discovered only with molecular tools. We analyze genetic diversity within one morphospecies, the ecologically important freshwater amphipod *Gammarus fossarum*. In accordance with previous studies, we find huge genetic divergence, indicating the presence of at least three cryptic species in Central Europe. The species are spatially sorted, suggesting that geographical location is indicative of the species present. Using microsatellite analyses, we find high between-population differentiation in one cryptic species, whereas a second cryptic species shows much less differentiation at a similar geographical scale. These data suggest either general differences in their biology (e.g. population sizes, dispersal abilities) or a recent range expansion of one species compared to long-term persistence of the other. The observed genetic structure may be indicative of adaptive divergence and reproductive compatibility between populations. We conclude that realistic biodiversity estimates for conservation as well as basic research need to consider the potentially surprising amount of diversity that can be hidden within one morphospecies.

Dating the models: arthropod macroevolutionary events and a revision of model genomic species' divergences

Christopher W. Wheat & Niklas Wahlberg

University of Exeter, UK

While advances in phylogenomics have begun to clarify the evolutionary relationships among arthropods, parallel advances in relaxed clock molecular dating are needed to investigate the Cambrian origins of arthropods, and assess macroevolutionary events such as the colonization of land and the evolution of flight and complete metamorphosis. Additionally, the 25 arthropod genomes currently available have yet to be integrated into a large phylogenomic study, leaving what is arguably the largest fraction of the research community without a robust phylogenetic and temporal foundation. Here, incorporating the current and emerging model genomic systems into a large scale phylogenomic study (122 taxa, 62 genes), we used a Bayesian relaxed molecular clock to simultaneously reconstruct robust phylogenetic relationships, and the absolute times of divergences, among the arthropods with a focus on the model genomic species. We also conducted simulations to assess whether our analysis could detect a true Cambrian explosion had it occurred. Our analysis and simulations suggest a Precambrian origin of the arthropods following the last 'snowball earth' glaciation event of the Ediacaran (635 Mya), and significantly alter the generally accepted divergence times among established model genomic species. These findings provide an essential foundation for macroevolutionary and comparative genomic study of the Arthropoda.

Investigating the mating success of honeybee queens in a managed apiary in mid-Wales

Ian Williams, David Wainwright & Anita Malhotra

Prifysgol Bangor University, UK

One explanation for the increasingly-observed phenomenon of "queen failure" is poor mating success in the cool, wet, summers experienced in recent years. Virgin queens leave the relative safety of their nests and fly to drone congregation areas (DCAs) to mate. They may visit a DCA one or more times to couple on the air with multiple males (drones). Poor weather can prevent queens from mating with enough drones, leading them to fail after a season or two instead of the normal three or four. We investigated how weather might influence the mating success of honeybees at a managed apiary in mid-Wales. Thirty test-queens were raised during the summer of 2009. These virgin queens were introduced into mating hives adapted to facilitate the observation of mating flight behaviour. Records were taken of the prevailing weather during this time. Sealed brood was sampled from hives with successfully laying queens about four weeks after mating. The degree of paternal variation within each sample was assessed using microsatellite DNA markers, and the correlation between mating performance and the weather conditions during the mating period assessed.

The effects of demography and linkage on the estimation of selection and mutation parameters

Kai Zeng & Brian Charlesworth

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We explore the effects of demography and linkage on a maximum likelihood (ML) method for estimating selection and mutation parameters in a reversible mutation model. This method assumes free recombination between sites and a randomly mating population of constant size, and uses information from both polymorphic and monomorphic sites in the sample. Two likelihood ratio test statistics were constructed under this ML framework – LRT-gamma for detecting selection and LRT-kappa for detecting mutational bias. By carrying out extensive simulations, we obtain the following results. When mutations are neutral and population size is constant, LRT-gamma and LRT-kappa follow a chi-squared distribution with one degree of freedom regardless of the level of linkage, as long as the mutation rate is not very high. In addition, LRT-gamma and LRT-kappa are relatively insensitive to demographic effects and selection at linked sites. We find that the ML estimators of the selection and mutation parameters are usually approximately unbiased, and that LRT-kappa usually has good power to detect mutational bias. Finally, with a recombination rate that is typical for *Drosophila*, LRT-gamma has good power to detect weak selection acting on synonymous sites. These results suggest that the method should be useful under many different circumstances.

Molecular phylogeography of the blood pheasant

Xiangjiang Zhan, Yifang Zheng , Fuwen Wei, Chenxi Jia & Michael W. Bruford

Cardiff University, UK

The role of Quaternary ice ages in forming the contemporary genetic structure of populations in the areas surrounding the Tibetan Plateau is debated yet, and has, to date, remained largely unstudied. We analysed the genetic structure of an alpine forest-associated galliforme bird, the blood pheasant (*Ithaginis cruentus*) to infer its phylogeographic history. We detected three genetic lineages and four current population groups. By comparing molecular with paleovegetation data, we inferred that glaciations during the Pleistocene have indeed had a major impact upon the current genetic diversity of this species. We used coalescent approaches to simulate the demographic history of the species and the most likely scenarios infer retraction of populations to different refugia during the first three glacial periods, but persistence during the last glacial maximum. Although analysis based on a plumage related gene showed that divergent selection may have contributed to current patterns of intra-specific diversity, demographic isolation is inferred to have played a more dominant role.

Poster Abstracts

Dissecting the causes of rate variation in the molecular clock

Veronica Comper, James Cotton & Richard Nichols

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Molecular-dating techniques can enable us to estimate the ages of important evolutionary events and can allows us to study the evolutionary history of related species when a fossil record is absent or poor. However, these techniques assume that molecular evolution occurs at a steady rate over time. Variation in this clock has been observed not only between species but also between genes and sections of genes. This project tries to model the molecular clock and tries to understand the causes of this variation. When the causes are found they could be incorporated into new molecular-dating techniques and hopefully will enable us to more accurately estimate evolutionary history.

The NERC Biomolecular Analysis Facility at Sheffield

Deborah Dawson

University of Sheffield, UK

The NERC Biomolecular Analysis Facility - Sheffield (NBAF-S) aims to make state-of-the-art molecular genetics facilities and training available to the UK community in the science areas that fall under the remit of the Natural Environment Research Council (NERC). The Facility was previously known as the Molecular Genetics Facility (MGF).

To date, the main call on the Facility is for the development and application of genetic markers for use in population genetics and behavioural ecology. The service is based on a well-proven arrangement, in which researchers visit the laboratory to complete their own analyses under the supervision of someone experienced in the required technology.

In most cases, the majority of the bench work will be carried out by visitors to the Facility under the supervision of Facility staff. Training will be provided, as appropriate. Facility staff will carry out those procedures that require a high level of training, such as the preparation of enriched microsatellite libraries, and may complete some smaller projects in their entirety.

If you would like any more details or wish to make informal enquiries regarding the feasibility of applying for access to the Facility please email Deborah Dawson (see List of participants, also website: http://www.shef.ac.uk/nbaf-s/).

Gene flow in gynodioecious *Beta vulgaris* ssp. maritima: pollen dispersal and heterogeneity in mating success inferred from parent–offspring analysis

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Variation among individuals in fitness traits is advocated as a major process driving the adaptive evolution in sexually polymorphic plants. In gynodioecious species, where females and hermaphrodites coexist, gender-specific differences in fitness are expected to explain the maintenance of females. In gynodioecious *Beta vulgaris* ssp. *maritima*, sex determination involves cytoplasmic male sterility genes (CMS) and nuclear restorers of male fertility, and both restored CMS hermaphrodites and non-CMS hermaphrodites occur. Using genotypic information on seedlings and on all flowering adults within structured populations, we investigated whether male fertility was influenced by genotypic and phenotypic differences, while taking into account the shape and scale of pollen dispersal and the geographical position of individuals. Along with spatially restricted pollen flow, we showed that male fecundity was significantly affected by individual size, pollen quality and cytoplasmic identity. Siring success of non-CMS hermaphrodites was significantly higher than restored CMS hermaphrodites, but strongly depended on the genetic neighborhood: male fertility of non-CMS hermaphrodites was significantly reduced by the occurrence of restored CMS hermaphrodites in their vicinity. Our results demonstrate a silent cost of restoration on male function, a condition theoretically expected to maintain a stable sexual polymorphism in gynodioecious species.

Early determinants of the genetic code

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The origins of the genetic code have been debated between adaptive and stochastic (frozen accident) evolutionary possibilities. The specificity with which the tRNA-synthetase molecules charge tRNAs with their cognate amino acids, and that the interaction between these molecules do not involve the anticodon region of the tRNAs, suggested that the genetic code was determined by the co-evolution between tRNAs and synthetases precursors. I will present a model for such a system, based on chemical kinetics inside a protocell, considering that the tRNA precursors are short hairpin replicators (as revealed by sequence comparison) forming a hypercycle, and where rybozymes with the synthetase activities catalyze the charging of the tRNAs. The chemical constants for the amino-acylations depend on the recognition of specific patterns of the tRNA hairpin sequences by the synthetases. These patterns might confuse different tRNAs, resulting in wrong aminoacylations. Natural selection, acting over a population of protocells, favours those with lesser mis-aminoacylations. I describe the evolution of the two different families of synthetases, which nowadays, recognize their tRNAs through two particular modes. In addition, it is possible to hypothesize which aminoacid inclusions to the early code might have been adaptive, or fixed by random selection.

Modeling speciation history: isolation and gene flow between house mouse subspecies inferred using approximate Bayesian computation (ABC).

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Understanding the speciation process requires to appraise not only patterns of gene flow between incipient species but its distribution in time. The two European subspecies of the house mouse (*Mus musculus domesticus* and *M. m. musculus*) are thought to have diverged in allopatry before they expanded into Europe and met secondarily, showing partial reproductive isolation. However, the history and geography of this divergence are yet poorly understood. We used an approximate Bayesian computation (ABC) framework to analyze their sequence variation at 64 autosomal loci. We compared 8 demographic scenarios with different explicit hypotheses concerning the presence and timing of gene flow. Results clearly reject strict isolation or continuous migration. Instead, they strongly support a model with a long isolation period of at least 700,000 generations preceding the advent of gene flow, which started around 200,000 generations ago. So, most of the genetic incompatibilities are likely to have accumulated in allopatry. On this basis, we propose an explicit geographical scenario for the formation of the subspecies which, after a long period of differentiation, would have met secondarily in the Middle East (presumably Iran) and partially mixed there before colonizing the periphery of this region, to ultimately expand over Europe.

Identifying selection pressures on Conserved Non-coding Elements (CNEs) in the human genome via analysis of Single Nucleotide Polymorphisms (SNPs) in the HapMap Populations

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CNEs are a set of ~7000 conserved non-coding regions of the genome, identified by whole genome comparison between human and *Takifugu rubripes* (Japanese Pufferfish). Arranged in clusters around genes regulating transcription and development (trans-dev genes) in vertebrates, some CNEs act as tissue-specific enhancers during embryonic development and are candidates for a network of cis-regulatory modules (CRMs). Their absence in invertebrates and characteristic clustering around trans-dev genes suggest that they have played in important role in the evolution of vertebrate embryonic development. Multiple sequence alignments of CNEs among different species show variable and non-variable regions (i.e. 100% sequence identity). Allele frequency spectra are expected to show characteristic differences between regions under purifying selection and at neutral loci. Here I report a preliminary analysis of the allele frequency spectra of single nucleotide polymorphisms (SNPs obtained from the International HapMap project). Significant differences were found between the spectra for SNP found in each of the following categories of DNA sequence: (1) Conserved Noncoding Elements (2) Noncoding Regions (3) Non Synonymous Sites (4) Synonymous Sites. The greater number of rare alleles in CNEs, Non Synonymous and Synonymous sites could be a signature of purifying selection.

Introducing MSMS: A coalescent simulator including Selection.

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We have implemented a coalescent simulation program for a structured population with selection at a single diploid locus. The program includes the functionality of the simulator {\it ms} to model population structure and demography, but adds a model for deme- and time-dependent selection using forward simulations. The program can be used, e.g.\, to study hard and soft selective sweeps in structured populations or the genetic footprint of local adaptation. The implementation is designed to be easily extendable and widely deployable. The interface and output format are compatible with {\it ms}. Performance is comparable even with selection included.

Triploid female production in an ant: investigating the causes and consequences

Richard Gill & Rob Hammond

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Haplodiploid sex determination (HDSD), as found in the Hymenoptera, is often based on a single-locus complementary sex determination system (slCSD) where heterozygous individuals develop into females and hemizygous individuals into males. Reduced genetic variation at slCSD or inbreeding leads to an increased likelihood of homozygosity resulting in the production of diploid males. Diploid males are often non-functional, being either inviable or developing as sterile males, and are therefore a genetic load. Models assuming such non-functionality show that the likelihood of population extinction is increased by an order of magnitude over that found for diplodiploids under inbreeding (Zayed & Packer 2005). We show contrary to the assumptions of this model diploid males in the ant *Leptothorax acervorum* can be fertile, and furthermore, that queens mated to diploid males can produce fully functional triploid workers. We found an appreciable proportion of colonies with triploid workers in populations of *L. acervorum* from Japan and Spain suggesting that some social insect populations can sustain a large diploid male load. We further discuss the mechanism of colony foundation and suggest it is crucial in determining the effective genetic load that diploid males have on social insect populations.

Characterising the phylodynamics of a pandemic as it emerges

Jessica Hedge & Andrew Rambaut

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The 2009 H1N1 pandemic was unprecedented in its depth and coverage of surveillance and by June 2010, over 1800 virus genomes had been sequenced. We use Bayesian phylogenetics to estimate three important genetic and epidemiological parameters to charaterise the pandemic as it broke out (evolutionary rate, date of the outbreak and the basic reproductive ratio, R0). We show that after the sequencing of the first ~100 virus genomes in early June 2009, the accuracy of our estimates remains constant and the addition of further sequencing only improves precision. Similar results were found in an analysis of seasonal H1N1 outbreak in North America and suggests that sufficient genetic diversity is present in the first 100-150 genomes sequenced to characterise both outbreaks using these three parameters. Further work will address whether the accuracy of these estimates is provided by the initial sequence diversity or the number of sequences analysed.

Cold-seeking Behaviour in *Drosophila*: Consequences for Host and Pathogen

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The consequences of natural infections are the results of complex interactions between host, pathogens as well as their external environments. While most infection studies examine host immune system under standardized laboratory conditions, their results might not be generalisable because they fail to consider host behavioural responses, which could dramatically alter the dynamics of immune response and the consequences of infection. Altered temperature-seeking behaviours in infected animals have been documented for many invertebrates and could play a role in regulating immune responses to ongoing infections. Here, we present results from studies using *Drosophila melanogaster* and *Metarhizium robertsii*, a common entomopathogenic fungus. We first report that wild type fruit flies infected with *M. robertsii* prefer cooler temperatures compared with uninfected controls, in contrast to behavioural fevering reported in other insects. We then show that the colder temperature preferred by infected flies significantly enhanced host survival, and recent preliminary results suggest that this could translate into higher lifetime reproductive success. Together, these results highlight that we cannot understand the dynamics and consequences of natural infections without incorporating host decision-making and behavioural modifications in our experiments.

Genetics of Sterility in a Grasshopper (*Chorthippus parallelus*) Hybrid Zone

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Identifying the loci involved in hybrid incompatibilities is a broad goal of speciation research. By identifying the functional classes of genes and the specific forces driving their divergence across species, we can come to understand their contribution to the evolution of new species. Two sub-species of the meadow grasshopper *Chorthippus parallelus* come into contact and hybridise in the Pyrenees Mountains. Crosses between sub-species produce fertile F1 females and sterile F1 Hybrid males with dysfunctional testes. This incompatibility is likely to result from negative epistatic interactions (Dobzhansky-Muller model). Within the hybrid zone, grasshoppers display intermediate phenotypes. Clines in morphological and behavioural characteristics have been observed spanning the hybrid zone. By using back-crossing experiments, clines for sterility have also been mapped (Shuker et al. 2005). Single Nucleotide Polymorphism markers have been developed for both candidate and putatively neutral loci and clines mapped across the hybrid zone. Here, we present the results from this study.

Non-random gene loss from the *Drosophila miranda* neoY chromosome

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Suppressed recombination leads to the degeneration of an evolving Y chromosome. However, it is not known whether gene loss is a largely random process and primarily driven by the order in which mutations occur, or whether certain categories of genes are lost less quickly than others; the latter would imply that selection counteracts the degeneration of Y chromosomes to some extent. In this study, we investigate the relationship between putative ancestral expression levels of neoY-linked genes in *Drosophila miranda* and their rates of degeneration. We use RNA-Seq gene expression data of neoY homologs in *Drosophila pseudoobscura* to show that genes that have become non-functional on the *D. miranda* neoY had, on average, lower ancestral expression levels than genes with intact reading frames. We also show that male-biased genes are retained for longer on the neoY compared to female-biased genes. Our results imply that gene loss on the neoY is not a purely random mutation-driven process. Instead, selection is, at least to some extent, preserving gene function of genes that are more costly to lose, despite the strongly reduced effective population size of the neoY.

Dynamics of the SNP frequency spectrum

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Testing polymorphism data with statistics such as Tajima's D or Fu and Li's test belong to the standard repertoire of population genetics. Achaz (2009) showed that those tests can be reduced to particular weighting schemes of differences of the frequency spectrum of alleles. Some theoretical results about constructing optimal tests relative to a given evolutionary scenario have recently been published by Ferretti et al. (2010). However, forward in time simulations of typical scenarios (e.g. selective sweeps) suggest that further gains in statistical power remain limited. We tracked the frequency spectrum and moments of the classic test statistics as a function of time. Furthermore, we investigated the frequency spectrum under recurrent selective sweeps.

Modeling Evolution of CRISPR spacers

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CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) is an adaptive heritable immune system found in Eubacteria and Archaea. The system consists of a number of CRISPR associated (CAS) proteins and an array of repeats and spacers - the later represent the viral/plasmid targeting sequences and the system functions in an analogous way to the eukaryotic siRNA system. The length and content of the spacer array varies considerably among individuals within species (suggesting a rapid arms race) and it has been suggested that there is a selective cost, in the absence of parasites, associated with maintaining these arrays. Therefore, the rate at which spacers are gained and lost from these arrays provides an insight into the evolutionary dynamics of host-parasite interactions. To this end we modeled spacer gain and loss as a continuous-time Markov process along the phylogeny. The maximum-likelihood framework allows us to estimate the overall rates of gain and loss of spacers, relative evolutionary rates of viral and plasmid spacers, and how these differ among bacterial species. We evaluate different models by simulation and the analyze bacterial data sets.

P element target preferences in natural strains

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Transposable elements (TEs) are mobile DNA sequences that are a source of mutations and target specific sites. The natural target preference of most TEs is unknown and is inferred after the insertion event occurred. Using genome resequencing data from 176 strains of *Drosophila melanogaster* gathered by the DGRP project we were able to identify 11,976 TE insertions in 8025 new insertion sites that can be used to decode the natural target preference for DNA, LTR and LINE elements in this species. These insertions are not present in the reference strain and therefore represent recent insertion events and reveal the genomic context in to which they inserted. The insertions are non-uniformly distributed with some elements showing a greater degree of occupancy in the same insertion site. Both Illumina and 454 sequencing platforms showed consistent results in terms of target site duplication (TSD) and target site motif (TSM) discovery. TSMs typically extend the TSD and are palindromic for both DNA and LTR elements whose palindrome centre varies according to the length of the TSD. Additionally, we found that TEs from the same subclass present similar TSDs and TSMs. Using the P-element as a benchmark, we show that there is overlap in target site preferences between artificial and natural insertion events. Our results demonstrate the utility of population genomics data for better understanding the targeting preferences of TEs in the wild.

DNA barcoding of diapausing stages of two rotifer genera as a taxonomic tool

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The highly variable and unpredictable environments in Mediterranean ponds are reflected in the seasonal and interannual variations in their zooplanktonic communities. In such fluctuating environments resting egg banks constitute an ecological and evolutionary reservoir that offers an invaluable tool for the study of biogeography, biodiversity, evolutionary ecology, paleolimnology, and community and population ecology. However, tools for taxonomic identification of dormant propagules are limited, so that researchers need to resort to experimental hatching for identification purposes, a method with inherent biases. An important breakthrough to investigate the dormant biodiversity in Mediterranean ponds would be the development of molecular tools for the direct identification of resting eggs. Here we have applied DNA barcoding technique to two Rotifers genera *Brachionus* and *Keratella* from two coastal ponds (Dulce and Santa Olalla, Doñana National Park) found in the water column and sediments. We extracted individual resting eggs DNA using HotSHOT and sequenced the PCR amplifications from the mitochondrial gene cytochrome c oxidase I (COI). We show how DNA barcoding makes possible to assign unidentified resting eggs to the correct species. We show that Molecular Barcoding can identify a species in their many life stages, from eggs to adults.

RAD sequencing for population genomics of *Anopheles gambiae* mosquitoes.

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Sequencing of RAD tags (Restriction-site-associated DNA tags) allows many individual samples to be barcoded and multiplexed on one Solexa lane with good coverage of each tag, in effect doing SNP discovery and genotyping in one experiment. The coverage and number of tags depends on the genome size and the restriction enzyme used. We have attempted RAD sequencing on 72 wild caught *Anopheles gambiae* individuals of three different species. The enzyme SbfI was used to give approx. 7500 70bp RAD tags per individual. Successful RAD sequencing libraries were made from all 72 samples. An average of 566,316 reads were generated per individual giving an average coverage of 75x. Initial alignment of An. gambiae s.s. data to the PEST genome indicates that in most samples at least 72% of tags were of *An. gambiae* origin. One exception shows very high levels of tags which align to human and cow genomes suggesting contamination from recent blood meals. The RAD tags will be used for population genomic analysis.

Tracking tigers in Sumatra

Tola Oni

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Indonesia has been identified as one of the key areas for the range-wide recovery of tigers. Current initiatives seek to identify the distribution of tigers, prey species and the associated anthropogenic threats across Sumatra. These studies provide an unrivalled opportunity to examine the impact of human disturbance and habitat type on the distributions of Sumatran tigers and other threatened mammal species. In addition to collecting data on the secondary signs (footprints etc) of tigers, prey species and human activities, field teams are collecting and preserving tiger faeces for genetic analysis. My research will focus on the analysis of microsatellite data to provide estimates of population structure and patterns of regional variation. Ultimately, this will allow us to predict the impact of current patterns of landscape change on the viability of the tiger populations across the island.

Conservation genetics of the critically endangered hawksbill turtle

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University of East Anglia, UK

Genetic techniques offer a powerful means for investigating previously unknown aspects of species' life histories. In our ongoing study, we are applying these techniques to the critically endangered hawksbill turtle *Eretmochelys imbricata*, a species that has experienced a substantial decline in its global population over the last century but about which very little is known. Our primary research areas concern mating behaviour, population connectivity, and genetic health of our focal population in the Seychelles. Using 30 variable microsatellite loci, we will address specific questions that include the number of males a female typically mates with, the size of the genetically effective population, and the effect of heterozygosity on nest hatching success. By incorporating mitochondrial sequence data from samples collected by our collaborators, we will also address questions relating to population structure, including the strength and spatial scale of structure, and the role of sex-biased dispersal in shaping turtle population genetics. Though the project focuses on hawksbills in the western Indian Ocean, our results are likely to have implications for understanding and conserving marine turtles well beyond these geographic limits.

Unwinding coiling dimorphism in Japanese land snails

Paul Richards

University of Nottingham, UK

Snails are excellent models for studying the evolution of left-right asymmetry. The fact that several taxa are dimorphic for coiling direction means that the underlying gene(s) may be mapped, and that the selective processes acting on coiling variants can be investigated. New coiling variants result from change at a single locus exhibiting delayed maternal inheritance. A new variant may be unable to mate with the existing one, because of the asymmetric positions of their genitalia. Modelling suggests the combination of asymmetry-driven reproductive isolation and delayed inheritance of the causal gene could, under rare circumstances, lead to 'single-gene speciation'. Mitochondrial DNA phylogenies for the Japanese land snail genus *Euhadra* are consistent either 'single-gene speciation' or gene flow between recently diverged clockwise and anticlockwise coiling species. I present new mitochondrial DNA data, which particularly focuses on populations where species of opposing coil direction coexist, including sequences from previously unsampled locations. I plan to extend this research using Restriction Site Associated DNA (RAD) genotyping to construct a high resolution nuclear DNA phylogeny to compare with the existing mitochondrial data, but also to identify candidate loci linked to the unidentified coiling gene.

Initial indications of stock differentiation in the genus Loligo along the southwest Atlantic coastline

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With the increase in exploitation of fisheries resources and the reduced abundance of current target species the so called 'unconventional' marine resources, of which cephalopods form a large part, have started to gain importance in the fisheries markets. A total catch of 3.3 million tonnes was registered in 2001, corresponding to 3.6% of marine products in this year. Both oceanic and coastal squid species form more than 70% of the total capture of cephalopods, with a very large proportion represented by the Genus *Loligo*, where curiously the majority of individuals disembarked are not identified to species level. In Brazil, oly the southern and southeastern regions have fleets which target cephalopods, where the species *L. plei* and *L. sanpaulensis* are the most abundant in catches. At the present time there are no records of the use of molecular markers for squid species in the southwestern Atlantic, with the exception of *L. gahi* from the Falkland Islands. As such the most targeted species lack any stock analysis from a molecular standpoint and genetic diversity is unknown in general. We present the first identification of genetic lineages of the main target species *L. plei* using sequence data for the barcoding gene CO1. Initial results suggest differentiation of stocks in northern and southern Brazilian waters. Further analysis with nuclear genes is underway to confirm this finding and help estimate variability within and between regions.

Population Genetics of Edible Crab in the Irish Sea

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Edible crab (*Cancer pagurus*) is of high economic value to the UK and Ireland and is being exploited with increasing intensity due to the decline of fin-fisheries. As part of an EU project (SUSFISH) to inform sustainable development of Irish Sea shellfisheries for the next 50-100 years, we aim to determine the effective population size and genetic structure of *C. pagurus* populations in this area and to establish the extent to which they are self-recruiting. Haemolymph will be collected from 50 adult *C. pagurus* from each of six locations within the Irish Sea; three off the coast of Wales (north, mid and south) and three off the coast of Ireland (north, mid and south). Genomic DNA will be extracted from the haemolymph and 12 species-specific microsatellite markers will be used to measure genetic diversity and infer population structure.

Gene flow in mangroves: An inter-species comparison

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Mangrove forests are a unique ecosystem in the sense that all true mangroves are hydrochoric and have the capability for long distance propagule dispersal. There is a broad spectrum of hydrochory characteristics and pollination syndromes among mangrove species. Whether these differences in reproductive ecology translate into varying degree and pattern of gene flow remain largely unknown. This project is a multi-scale, multi-species study on gene flow in mangroves. The four selected species—*Avicennia alba*, *Sonneratia alba*, *Bruguiera gymnorrhiza* and *Rhizophora mucronata*—differ greatly in reproductive biology. The aim is to understand how reproductive strategies affect gene flow at two spatial scales—within population and among populations along the same coastline. Understanding gene flow variability among species and the intrinsic (biological) and extrinsic (environmental) factors behind it is crucial for assessing the genetic susceptibility of a given species towards habitat loss and the potential of recovery. Here, the study design for both spatial scales is discussed. Preliminary results for spatial genetic structure comparison between *A. alba* and *R. mucronata* in a population from Singapore is presented.

Non-Random Genome Organization and the Expressional evolution of retrogenes

Elaine Wilkin

Retrotransposition, in which a processed mRNA molecule is copied by reverse transcription and inserted in to the genome, is an important mechanism by which gene creation occurs. It has been demonstrated that many retrogenes acquire testis specific expression profiles in contrast to the more ubiquitous expression profiles of their progenitor genes. How, and why, these new copies acquire this specific pattern of expression remains unclear. Retrotransposition mechanistically decouples retrogenes from their ancestral cis-acting regulatory regions and it has therefore been suggested that characteristics of the genomic region into which a retrogene is inserted may be a significant factor influencing the life history of that gene. We used an adjacent gene model to identify significant occurrences of colocalization (clustering) of (i) testis overexpressed genes and (ii) genes upregulated during the post-meiotic stage of spermatogenesis relative to earlier stages of spermatogenesis. We then assessed associations between retrogene location, expression and the genomic neighborhoods within which they reside and found that retrogenes with male biased expression are significantly associated with genomic regions enriched for male-biased expression. We found no similar location bias for transposable elements and therefore do not favor insertional bias as a cause of this association. We propose that the genomic region into which a retrogene inserts is influential in the early evolution and subsequent retention of retrogenes in the genome.
