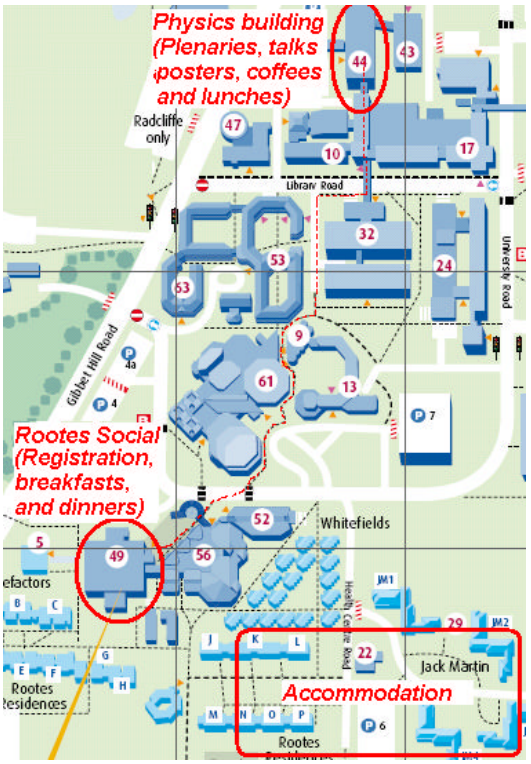
Welcome to the 41st Population Genetics Group Meeting

Monday 17th of December - Thursday 20th of December
University of Warwick conference centre

Conference website: http://www.popgroup.org



Registration is in the Rootes Social building. The same building will be used for breakfasts, dinners and the conference dinner. There is also a bar in that building that should be open until midnight. All the talks, posters and buffet lunches will be in the Sciences Physics building. The walk between the Physics and Rootes Social buildings takes about 5 min (note that the library road is crosses over a footbridge).

Internet is accessible via wireless, or via several PC computers in the Rootes Social building.

Parking is available at the car parks 5 and 6

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Programme outline

Monday the 17th of December					
17:00-22:00	**Arrival and registration (Rootes Social building)**				
19:00	**Dinner (Rootes Social building)**				
	LT-A		**LT-B**		**LT-C**
Tuesday the 18th of December					
9:00-9:50	Plenary: Chung-I Wu				
10:00-10:20	Mohamed Noor	**10:00-10:20**	Mark Beaumont	**10:00-10:20**	Vini Pereira
10:20-10:40	Audrey Chang	**10:20-10:40**	Katalin Csillery	**10:20-10:40**	Martin Carr
10:40-11:00	Marianne Elias	**10:40-11:00**	Konrad Lohse	**10:40-11:00**	Louise Johnson
			coffee		
11:40-12:00	Irene Keller	**11:40-12:00**	Laurence Loewe	**11:40-12:00**	Michel Bruford
12:00-12:20	Paris Veltsos	**12:00-12:20**	Eric Bazin	**12:00-12:20**	Einar Arnason
12:20-12:40	Amy Sherborne	**12:20-12:40**	John Pannell	**12:20-12:40**	Sam Cotton
		lunch (Physics building, next to posters)			
14:00-14:20	Mathieu Joron	**14:00-14:20**	Jitka Polechova	**14:00-14:20**	Deborah Charlesworth
14:20-14:40	Chris Thorogood	**14:20-14:40**	Kermit Ritland	**14:20-14:40**	Barbara Mable
14:40-15:00	Patrik Nosil	**14:40-15:00**	Samuel Dobbie	**14:40-15:00**	Jesper Bechsgaard
			coffee		
15:40-16:00	Ren Chao Zhou	**15:00-15:20**	Marc Stift	**15:00-15:20**	Jean-Baptiste Leducq
16:00-16:20	Magdalena Zarowiecki	**16:00-16:20**	Mattias Jakobsson	**16:00-16:20**	Stacey Lee Thompson
16:20-16:40	Nikolai Mugue	**16:20-16:40**	Luzie Wingen	**16:20-16:40**	Pernilla Vallenback
16:40-17:00	Andrea Harper	**16:40-17:00**	Greg Hurst	**16:40-17:00**	Claire Raisin
17:00	**Poster session (Physics building)**				
19:00	**Dinner (Rootes Social building)**				
Wednesday the 19th of December					
9:00-9:50	Plenary: Laurence Hurst				
10:00-10:20	Daniel Jeffares	**10:00-10:20**	Brian Charlesworth	**10:00-10:20**	Katy Morgan
10:20-10:40	Tobias Warnecke	**10:20-10:40**	Stephan Hutter	**10:20-10:40**	Mathilde Cordellier
10:40-11:00	Richard Buggs	**10:40-11:00**	Warren Booth	**10:40-11:00**	Jemma Somerville
			coffee		
11:40-12:00	Katie Tindall	**11:40-12:00**	Darren Obbard	**11:40-12:00**	Kanchon Dasmahapatra
12:00-12:20	Paul Sharp	**12:00-12:20**	Clare Marsden	**12:00-12:20**	Keith Gardner
12:20-12:40	Shuhei Mano	**12:20-12:40**	Kathrin P Lampert	**12:20-12:40**	Sara Goodacre
		lunch (Physics building, next to posters)			
14:00-14:20	Brent Emerson	**14:00-14:20**	John Grahame	**14:00-14:20**	Courtenay Mills
14:20-14:40	Alex McCarthy	**14:20-14:40**	Heidi Seears	**14:20-14:40**	Stephen Ansell
14:40-15:00	Maxim Kapralov	**14:40-15:00**	Kate Ciborowski	**14:40-15:00**	Ismael Khatab
			coffee		
15:40-16:00	Leonard Nunney	**15:40-16:00**	Sophia Ahmed	**15:40-16:00**	Adele Grindon
16:00-16:20	Bárbara Negre	**16:00-16:20**	Benoit Pujol	**16:00-16:20**	AnaPrevisic
16:20-16:40	Konstantin Popadin	**16:20-16:40**	Tim Bray	**16:20-16:40**	Chris Dixon
16:40-17:00		**16:40-17:00**		**16:40-17:00**	
17:00	**Business meeting / Heredity board meeting (Lect. Theatre B in the Physics building)**				
19:30	**Conference dinner (Rootes Social building)**				
Thursday the 20th of December					
9:00-9:50	Plenary: David Waxman				
10:00-10:20	Susan Armstrong	**10:00-10:20**	Paul Rymer		
10:20-10:40	Dmitry Filatov	**10:20-10:40**	Peter Wandeler		
10:40-11:00	Jan Engelstaedter	**10:40-11:00**	Ryan Woods		
			coffee		
11:40-12:00	Richard Nichols	**11:40-12:00**	Arjen Van 't Hof		
12:00-12:20	Vera Kaiser	**12:00-12:20**	Corneel Vermeulen		
		lunch (Physics building, next to posters)			

Tuesday the 18th of December

Plenary (LT-A):

9am Chung-I Wu Microevolution between species in relation to the evolution of microRNA genes

LT-A	LT-B	LT-C
10:00-10:20 Mohamed Noor Recombination, diversity, and divergence in the *Drosophila pseudoobscura* species subgroup	**10:00-10:20 Mark Beaumont** Inferring selection coefficients and other parameters from temporal and spatial data	**10:00-10:20 Vini Pereira** The effect of new transposable element insertions on gene expression profiles
10:20-10:40 Audrey Chang Epistatic interactions modify dominance of loci causing hybrid male sterility between *D. persimilis* and *D. pseudoobscura bogotana*	**10:20-10:40 Katalin Csillery** How to test a biologically meaningful null hypothesis of no linkage disequilibrium in finite population samples?	**10:20-10:40 Martin Carr** Three potentially functional families of LTR retrotransposons are present in the genome of the choanoflagellate *Monosiga brevicollis*
10:40-11:00 Marianne Elias Speciation out of the Andes: patterns of diversification of neotropical ithomiine butterflies	**10:40-11:00 Konrad Lohse** How to measure starshape in genealogies? Summary statistics and demographic inference	**10:40-11:00 Louise Johnson** Evolution of a genome defence system
	11:00 – 11:40 Coffee	
11:40-12:00 Irene Keller The frequency of rDNA variants within individuals provides evidence of population history and gene flow across a grasshopper hybrid zone	**11:40-12:00 Laurence Loewe** The distribution of mutational effects on fitness within genes	**11:40-12:00 Michel Bruford** Pleistocene refugia, rivers and western lowland gorilla diversity in central Africa
12:00-12:20 Paris Veltsos Evidence of selection on rDNA in the *Podisma pedestris* hybrid zone	**12:00-12:20 Eric Bazin** Quantifying levels of adaptive divergence between populations from frequency data	**12:00-12:20 Einar Arnason** Environmental correlates and selection at the PanI locus in Atlantic cod
12:20-12:40 Amy Sherborne The genetic basis of inbreeding avoidance in house mice	**12:20-12:40 John Pannell** Overdominant selection at sex-linked loci and the long-term maintenance of males with hermaphrodite crustaceans	**12:20-12:40 Sam Cotton** Population consequences of environmental sex reversal
	12:40 – 14:00 Lunch	
14:00-14:20 Mathieu Joron Towards the identification of a butterfly colour-pattern supergene	**14:00-14:20 Jitka Polechova** Evolution of species range in spatially and temporarily varying environments	**14:00-14:20 Deborah Charlesworth** High DNA sequence diversity in pericentromeric genes of the plant *Arabidopsis lyrata*
14:20-14:40 Chris Thorogood Host-driven speciation in a parasitic plant	**14:20-14:40 Kermit Ritland** The use of higher-order gene identity coefficients in population genetic studies	**14:20-14:40 Barbara Mable** Genetic diversity in relation to ploidy and mating system in *Arabidopsis lyrata*
14:40-15:00 Patrik Nosil Heterogeneous genomic divergence during speciation	**14:40-15:00 Samuel Dobbie** Variability in disease prevalence stabilises host-parasite coevolution by generating density-dependent selection	**14:40-15:00 Jesper Bechsgaard** Adaptive introgression mediated by balancing selection at the self-incompatibility locus between *Arabidopsis lyrata and A. halleri*
	15:00 – 15:40 Coffee	
15:40-16:00 Ren Chao Zhou Contrasting ancestral and extant polymorphisms in *Sonneratia*	**15:00-15:20 Marc Stift** A new likelihood based method to test tetraploid inheritance models: Rorippa hybrids show inheritance patterns intermediate between disomic and tetrasomic	**15:00-15:20 Jean-Baptiste Leducq** Effect of balancing selection on spatial genetic structure within continuous populations: theory and empirical evidence from the self-incompatibility locus in *Arabidopsis halleri*
16:00-16:20 Magdalena Zarowiecki Ecological and geographical drivers of speciation in the *Anopheles sundaicus* (*Diptera*: *Culicidae*) species complex	**16:00-16:20 Mattias Jakobsson** CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure	**16:00-16:20 Stacey Lee Thompson** The applied population genetics of *Populus*: transgenes, exotic species, gene flow, markers, and more
16:20-16:40 Nikolai Mugue 'Mongrel dog' model of speciation and its implication for analysis of sympatric morphs	**16:20-16:40 Luzie Wingen** Long-distance dispersal and adaptation to host resistance in a heterogeneous environment	**16:20-16:40 Pernilla Vallenback** A natural transgenic plant
16:40-17:00 Andrea Harper 'Porous' species boundary between *Silene latifolia* and *S. dioica*	**16:40-17:00 Greg Hurst** Evolution in the fast lane: tales from male-killer/host interactions in the South Pacific	**16:40-17:00 Claire Raisin** Conservation genetics of the endangered Mauritius parakeet

17:00 Poster session (Physics building)

19:00 Dinner (Rootes Social building)

Wednesday the 19th of December

Plenary (LT-A):

9am Laurence Hurst Why isn't gene order random in eukaryotic genomes?

LT-A	LT-B	LT-C
10:00-10:20 Daniel Jeffares Comparative Plasmodium genomics and population genomics of the malaria parasite *Plasmodium falciparum*	**10:00-10:20 Brian Charlesworth** Components of genetic variance in female fertility in *Drosophila melanogaster* suggest contributions from alleles at intermediate frequencies	**10:00-10:20 Katy Morgan** Molecular phylogenetics and biogeography of the Neocellia series of Anopheles mosquitoes across Southeast Asia
10:20-10:40 Tobias Warnecke In high demand: Synonymous sites face conflicting selection pressures at exon-intron boundaries	**10:20-10:40 Stephan Hutter** Gene expression variation in African and European populations of *Drosophila melanogaster*	**10:20-10:40 Mathilde Cordellier** Ecological modelling and phylogeography of European freshwater snails: can we predict the impact of climate change?
10:40-11:00 Richard Buggs Preferential gene loss or retention following genome duplication in allopolyploid species of *Tragopogon* (*Asteraceae*).	**10:40-11:00 Warren Booth** Population genetic structure of a commensal insect pest in the agricultural environment	**10:40-11:00 Jemma Somerville** Fire ants in Australia: Determining the origin of *Solenopsis invicta* Buren (Hymenoptera: Formicidae)
	11:00 – 11:40 Coffee	
11:40-12:00 Katie Tindall LAPDOG - a tool for generation of orthologous nucleotide datasets and application of these datasets in genomic studies	**11:40-12:00 Darren Obbard** The evolution of TEP1, an exceptionally polymorphic immunity gene in *Anopheles gambiae*	**11:40-12:00 Kanchon Dasmahapatra** Can Pleistocene refugia explain current Neotropical biodiversity
12:00-12:20 Paul Sharp Leaping (or sliding?) between peaks of co-adaptation	**12:00-12:20 Clare Marsden** Characterising MHC variation in the endangered African wild dog (Lycaon pictus)	**12:00-12:20 Keith Gardner** Temperate forest refugia and postglacial expansion in Europe: the eastern story
12:20-12:40 Shuhei Mano The evolutionary rate of multigene families under concerted evolution	**12:20-12:40 Kathrin Lampert** MHC variability in a unisexual vertebrate	**12:20-12:40 Sara Goodacre** Endosymbiont infections and dispersal strategy of the money spider *Erigone atra*
	12:40 – 14:00 Lunch	
14:00-14:20 Brent Emerson Ancient DNA and the time dependancy of mutation rates	**14:00-14:20 John Grahame** Selection, sequences, phenotypes, and fitness in an intertidal snail	**14:00-14:20 Courtenay Mills** Population expansions in Australian estuarine Glassfish, *Ambassis marianus* (Günther 1880) and *Ambassis jacksoniensis* (Macleay 1881)
14:20-14:40 Alex McCarthy Pathogen evolution and disease emergence in carnivores	**14:20-14:40 Heidi Seears** Genetic diversity of the planktonic foraminifera in the Arabian Sea	**14:20-14:40 Stephen Ansell** Genetic discontinuity, breeding system change and population history of Arabis alpina in the Italian Peninsular and adjacent Alps
14:40-15:00 Maxim Kapralov Parallel length expansions in the thioredoxin h1 protein during an adaptive radiation in the Hawaiian plant genus *Schiedea*	**14:40-15:00 Kate Ciborowski** Spatio-temporal genetic variability in Spanish Atlantic salmon populations	**14:40-15:00 Ismael Khatab** Phylogeography of Eurasian Larix species inferred from nucleotide variation in two nuclear genes
	15:00 – 15:40 Coffee	
15:40-16:00 Leonard Nunney A clade-site method for detecting positive selection: dissecting the phylogenetics of adaptation	**15:00-15:20 Sophia Ahmed** Investigating patterns of temporal genetic variation in the freshwater bryozoan *Cristatella mucedo*	**15:00-15:20 Adele Grindon** The colonisation of Ireland: myths, mystery, and molluscs
16:00-16:20 Bárbara Negre Evolution of the achaete-scute complex in insects: recurrent duplication of proneural genes	**16:00-16:20 Benoit Pujol** Range expansion depletes heritability of a major plant life-history trait	**16:00-16:20 Ana Previsic** Phylogeography of caddisflies: identification of the processes underlying high diversity and endemism in the Balkans
16:20-16:40 Konstantin Popadin Life-history traits drive the rates of accumulation of slightly-deleterious mutations in mammalian coding elements	**16:20-16:40 Tim Bray** Unravelling complex admixture in livestock: approaches and application to the Dexter cattle breed	**16:20-16:40 Chris Dixon** Distribution is a poor predictor of infraspecific genetic variation in *Androsace* sect. *Aretia*

17:00 Business meeting / Heredity board meeting (Lect. Theatre B in the Physics building)
19:30 Conference dinner (Rootes Social building)
~22:00 Dancing party (Rootes Social building)

Thursday the 20th of December

Plenary (LT-A):
9am David Waxman Revisiting random genetic drift

	LT-A	LT-B	LT-C
10:00-10:20	**Susan Armstrong** Molecular cytogenetics of sex chromosome evolution in the genus *Silene*	**Paul Rymer** Mating patterns in fragmented landscapes: a case study of a neotropical tree	
10:20-10:40	**Dmitry Filatov** X vs autosomal comparison of DNA polymorphism in *Silene latifolia*	**Peter Wandeler** Matrilineal clusters reflect female philopatry in snow voles	
10:40-11:00	**Jan Engelstaedter** The degeneration of Y chromosomes through Muller's ratchet: A simulation study	**Ryan Woods** Connectivity in an ephemeral Australian river system: Population genetics meets otolith chemistry	
		11:00 – 11:40 Coffee	
11:40-12:00	**Richard Nichols** The inevitable ascent of Y chromosomes	**Arjen Van 't Hof** Mapping melanism in the peppered moth	
12:00-12:20	**Vera Kaiser** Hill-Robertson interference among strongly selected sites reduces their effects on linked neutral sites	**Corneel Vermeulen** The genetic basis of inbreeding depression: Case studies of adult lethality in Drosophila	
		12:20 Lunch	

Plenaries (all at 9am in the Lecture Theatre A in Physics)

Tuesday the 18th of December

Microevolution between species in relation to the evolution of microRNA genes

Chung-I Wu *and Jian Lu*
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Department of Ecology and Evolution University of Chicago Chicago IL 60637 USA

MicroRNAs (miRNAs) are small RNAs (19-24 nt) that regulate mRNAs post-transcriptionally. In animals, the number of miRNA genes is estimated to be 100 – 1000. Each miRNA may attenuate the expression of up to 150 target genes but the effect is of a modulation kind. The regulation is thus more akin to a rheostat (or dimmer) than an on-off switch. In this sense, the molecular mechanism of miRNA regulation is reminiscent of the diffuse genetic architecture underlying phenotypic differentiation between races or closely related species. Three topics will be covered. 1) Birth and death of miRNAs - We carried out deep-sequencing of miRNAs from three species of Drosophila, and obtained 150,000 sequences. We observed a large class of miRNA genes that are evolutionarily young, with a fixation rate of >10 new genes per million years (Myrs). Among them, only 2.4% eventually become functionally integrated into the genome. Our results suggest a very high birth and death rate of new miRNA genes, resulting in a very modest net gain of 0.3 miRNA genes per Myrs in Drosophila. 2) By comparing the divergence and polymorphism of 5 newly emerged miRNA genes, we infer that such miRNAs have undergone a long period of adaptive evolution (> 30 Myrs) and accumulated many changes before functional integration. 3) We studied the coevolution of miRNAs and their targets by using the transgenic technique on conspecific and heterospecific miRNA genes. The data suggest that miRNAs and their potential targets coevolve mostly by avoidance, as deleterious miRNA-target interactions outnumber beneficial ones. Hybrid incompatibility through aberrant miRNA-target interactions in the Muller-Dobzhansky framework was observed. miRNA genes as a class of regulatory molecules may be of relevance to microevolutionary processes.

Wednesday the 19th of December

Why isn't gene order random in eukaryotic genomes?

Laurence Hurst
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For a few years now it has been recognized that gene order in eukaryotes is not random. In particular, genes of comparable expression profile tend to cluster in genomes. In yeast, for example, highly co-expressed genes tend to cluster, while in mammals broadly expressed genes cluster. These findings suggest several new problems. First, is this clustering the result of natural selection or might it simply reflect leaky expression of neighbouring genes? Second, does clustering for co-expression explain all clustering? I shall present evidence that selection does act on gene order to maintain physical proximity of co-expressed genes. However, I shall also show that linkage per se ensures some degree of co-expression (even controlling for the similarity in transcription factor control) and only for the most highly co-expressed gene pairs need we suspect the action of selection. As regards the final issue, I argue that selection for minimization of noise in gene expression can explain many of the unusual features of the distribution of genes in the yeast genome, not least of which is the clustering of essential genes.

Thursday the 20th of December

Revisiting random genetic drift

David Waxman
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Department of Biology and Environmental Science School of Life Sciences The University of Sussex Brighton BN1 9QG Sussex UK

Random genetic drift is one of the key processes of population genetics and evolution. The single, most important approach to random genetic drift is the diffusion approximation. In this accessible talk I reconsider theoretical results in the literature concerning the diffusion approximation. Solutions of the diffusion equation will be discussed that differ from the accepted ones. These will be shown to be in greater accord with intuition and lead naturally to the way generalisations of existing results for fixation probabilities may be achieved.

Talks

Investigating patterns of temporal genetic variation in the freshwater bryozoan *Cristatella mucedo*
Sophia Ahmed, Mark Beaumont and Beth Okamura
e-mail: sophia.ahmed@reading.ac.uk
School of Biological Sciences Philip Lyle Tower, Whiteknights campus, University of Reading, Reading RG6 1BX, United Kingdom.

Cristatella mucedo is a commonly occurring species of the class *Phylactolaemata*, the freshwater bryozoans. They exist as sessile filter feeding colonies that reproduce mostly by asexual methods with brief periods of sexual reproduction. We have investigated temporal changes in allele frequencies of up to 12 microsatellite loci from four different locations and use this data to determine if temporal gene flow can explain the observed levels of genetic diversity.

Genetic discontinuity, breeding system change and population history of *Arabis alpina* in the Italian Peninsular and adjacent Alps
Stephen Ansell, Grundmann M., Russell S. J., Schneider H and Vogel J. C.
e-mail: s.ansell@nhm.ac.uk
Dept. Botany, Natural History Museum, Cromwell Road, London, SW7 5BD, United Kingdom

Arabis alpina is a widespread plant of European arctic and alpine environments and a close relative of Arabidopsis thaliana. It grows in all major mountain ranges within the Italian glacial refugia and populations were sampled over a 1,300 km transect from Sicily to the Alps. Diversity was studied in nuclear and chloroplast genome markers. Alpine populations had significantly lower levels of nuclear genetic variation compared to those in the Italian peninsular, and this is associated with a pronounced change in within-population inbreeding. Alpine populations are significantly inbred (F_{IS}= 0.553), potentially compatible with a breakdown in self-incompatibility system during leading edge colonisation. Italian peninsular populations are outbreeding (F_{IS}=0.076) and genetic variation is highly structured, consistent with independent local "refugia-within-refugia" and the fragmentation of an established population by Quaternary climate oscillations. With limited evidence of genetic exchange between the Alps and the Italian distribution ranges, and a strong pattern of isolation by distance, it appears the Alps functioned as a glacial sink for *A. alpina*, while the Italian peninsular remains a distinct and separate long-term refugium.

Molecular cytogenetics of sex chromosome evolution in the genus *Silene*
Susan J Armstrong, Elaine Howell, Constantinos Groutides, Reuben Harwood and Dmitry A. Filatov
e-mail: s.j.armstrong@bham.ac.uk
School of Biosciences, University of Birmingham, Birmingham B15 2TT, United Kingdom

Analysis of sex chromosomes in the plant *Silene latifolia* and its close relatives provides an opportunity to study the early stages of sex chromosome evolution. Adapting existing *Arabidopsis* cytogenetic techniques to Silene has enabled us to produce good quality meiotic and mitotic chromosomes suitable for fluorescence in situ hybridisation (FISH). Development of FISH during the last two decades has proved to be an invaluable tool in plants both for mapping single copy and repetitive DNA sequences. This approach has been instrumental in improving our understanding of the karyotype of *S. latifolia*. Currently we have a small number of probes from sex linked genes but have found that most are not large enough to give a signal that can be reliably detected by image analysis. We are attempting to generate further probes from these genes by PCR and also are screening a fosmid library to find other sex chromosome specific genes. Isolation of more plant sex-linked genes and their cytogenetic mapping with FISH will ultimately lead to a much better understanding of the processes driving sex chromosome evolution in this genus.

Environmental correlates and selection at the Pan I locus in Atlantic cod
Einar Arnason and Ubaldo Benitez Hernandes
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Institute of Biology, Sturlugata 7 Reykjavik IS-101 Iceland

The Pantophysin I (Pan I) of Atlantic cod, originally detected by Pogson as an outlier among anonymous cDNA loci and subsequently cloned and sequenced, shows all signs of selection at DNA sequence level. Two alleles that are defined by a single restriction site differ by a number of synonymous and non-synonymous nucleotides. They represent an ancient balanced polymorphism. We will briefly review the evidence and then present our results of a large scale study on genotypic and genic structure of populations in Icelandic waters. We have data from all measured and aged fish taken by Marine Institute Research Vessels in spring-spawning and fall-wintering-ground surveys over three years. There are clear correlations of allele frequencies with environmental factors, depth in particular, with a greater than 50% highly regular change in allele frequency in a depth range of a 100 meters. The effect of age and year-class and other variables is also examined. The results have implications for studies of the nature and strength of selection, in particular in high-fecundity organisms like cod.

Quantifying levels of adaptive divergence between populations from frequency data
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There is currently much interest in identifying loci under selection from genomic 'scans' of multiple loci. A number of different approaches have been developed (Nielsen, 2005, Annu. Rev Genet., 39:197). Some of them are dedicated to the detection of genes involved in local adaption (Beaumont and Nichols, 1996, Genetics, 153:2013; Vitalis et al., 2001, Genetics, 158:1811; Beaumont and Balding, 2004, Mol. Ecol., 13: 969). These methods methods have been quite widely used for detecting evidence of selection, particularly in non-model organisms (e.g. Bonin et al, 2006, Mol. Biol. Evol., 23:773; Vasemagi et al, 2005, Mol. Biol. Evol., 22:1067; Savolainen et al, 2006, Nature, 441:210).
We extend these approaches by using an other method that has come to be called 'Approximate Bayesian Computation' or ABC (Beaumont et al., 2002, Genetics, 162:2025). The idea is to measure a number of summary statistics from the genomic data and then perform a large number of simulations from a model, where the model parameters have values that are drawn from particular distributions. The summary statistics from the simulated data are compared with those in the real data, and, after a bit of manipulation, it is then possible to obtain the posterior ditribution of parameters of interest. Ideally these parameters should include selection coefficients. However models with selection are generally much more computationally time-consuming than neutral models, and so we deal with purely neutral models, and identify loci under selection by taking a hierarchical Bayesian approach, as used in, for example, Storz and Beaumont (2002, Evolution, 56:154). Thus we use ABC to fit a complex and realistic demographic model to the majority of loci, and identify those loci that do not fit the model.

Inferring selection coefficients and other parameters from temporal and spatial data
Mark Beaumont
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School of Biological Sciences, Philip Lyle Research Building, PO Box 68 University of Reading Whiteknights Reading RG6 6BX U.K.

An ongoing project is described where the general aim is to infer selection coefficients, recombination rates, and demographic parameters from genetic data sampled at different points in time. A long-term goal is to provide a framework for analysing ancient DNA data with a view to inferring selection and past demographic processes. Most current modelling methods for dealing with temporal data assume neutrality (e.g. Beaumont, 2003). A motivating data set comes from the snail Cepaea nemoralis, which has been surveyed at four genetic loci that control shell colour and banding patterns in 106 populations in 1961 and 1985 (Cain and Currey, 1961; Cowie and Jones, 1998; Cook et al., 1999). Results are given for a 3-locus model with dominance, epistasis and linkage, involving 9 phenotypes and 78 genotypes. Markov chain Monte Carlo is used to integrate over the unknown haplotype frequency trajectories, and thereby infer relevant parameters. There is some evidence of the effect of natural selection, and the potential confounding effects are discussed.

Adaptive introgression mediated by balancing selection at the self-incompatibility locus between *Arabidopsis lyrata and A. halleri*

Jesper Bechsgaard, Vincent Castric, Xavier Vekemans and Mikkel H. Schierup
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Department of Biological Sciences Ny Munkegade Building, University of Aarhus, 1540 DK-8000 Aarhus C Denmark

Reproductive barriers between recently diverged species are often incomplete with a certain amount of hybridization followed by introgression. Natural selection is typically considered a key factor preventing or promoting introgression, resulting in heterogeneous divergence across the genome. Documented examples of introgression affected by natural selection remain rare, and all involve directional selection. However, theory predicts that adaptive introgression might also occur for alleles at genes evolving under multi-allelic balancing selection. We test the prediction that alleles at the gene controlling pistil self-incompatibility specificity in two closely related *Arabidopsis* species introgressed for longer and at a higher rate than the genomic background. Polymorphism at this gene is largely shared, and we have identified 18 pairs of S-alleles that are only slightly divergent between the two species. Synonymous divergence between these "orthologous" S-alleles (KS=0.023) is about four times lower than the genomic background (KS=0.090). We used arguments based on coalescent theory to demonstrate that this difference cannot be explained by differences in effective population size between the two types of loci. We conclude that the lower divergence reflects higher introgression at the S-locus than at the rest of the nuclear genome, making this study the first documented example of adaptive introgression facilitated by balancing selection.

Population genetic structure of a commensal insect pest in the agricultural environment.

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The German cockroach, *Blattella germanica*, is a major pest of both the urban and agricultural (livestock) environments. One such agricultural system suffering heavy infestations is that of swine production within the United States. US Swine production is mainly by contract farms that produce the swine and are each then associated with larger vertical producers, responsible for providing breeding animals, semen for fertilization, and feed. Cockroaches may potentially spread through hitching rides on supply trucks from an infested central feed mill or warehouse belonging to a producer, to any farm within that producer's contractees, but not into other farms that are under another producer's contract. This theoretically may then result in a relative isolation of cockroaches along known routes of transport. Since these contracts are long-term arrangements, they may represent channels, as well as barriers, for cockroach dispersal. We hypothesis that combined with farm bio-security, the concept of this production system may result in long-term separation and genetic differentiation of cockroach populations along producer boundaries. In this study we apply both microsatellite markers and sequencing of the COII and 16S mtDNA genes in order to test this hypothesis, assessing the levels of genetic diversity and differentiation both between and among farms bound under vertical producers within the swine production system of North Carolina. The results of this study will facilitate a better understanding of the process by which genes spread within and between cockroach populations, including genes conferring insecticide resistance and behavioural aversion of baits and bait matrices.

Unravelling complex admixture in livestock: approaches and application to the Dexter cattle breed

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Understanding the dynamics of admixture in populations where genetic drift also contributes to patterns of diversity is a challenging yet important question, especially in minority livestock breeds, where small populations have been traditionally 'upgraded' using other breeds to regain popularity. The genetic structure of the Dexter, a minority breed with a complex demographic history, was investigated using microsatellite markers and a range of statistical approaches designed to detect both admixture and drift. Substantial variation and structure was observed in the Dexter and its diversity was compared with other European breeds. The relationships between breed lines and the putative ancestors of the Dexter breed were varied and the implications of demographic history and genetic drift are considered.

Pleistocene refugia, rivers and western lowland gorilla diversity in central Africa
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The role of Pleistocene forest refugia and rivers in the evolutionary diversification of tropical biota has been the subject of considerable debate. A range-wide analysis of gorilla mitochondrial and nuclear variation was used to test their role in shaping genetic diversity in current populations. Results revealed strong patterns of regional differentiation consistent with refugial hypotheses for central Africa. Four major mitochondrial haplogroups were evident with the greatest divergence between eastern and western gorillas. Coalescent simulations rejected a model of recent east-west separation during the last glacial maximum but were consistent with a divergence time within the Pleistocene. Microsatellite data also supported a similar regional pattern of structure. Signatures of demographic expansion were detected in eastern lowland and Gabon/Congo haplogroups and were consistent with a history of postglacial expansion from formerly isolated refugia. Although most mitochondrial haplogroups were regionally defined, limited admixture was also evident. Mantel tests revealed significant isolation-by-distance, however mitochondrial divergences also correlated with the distance required to circumnavigate intervening rivers, indicating a role for rivers in partitioning gorilla genetic diversity. More comparative data are needed to evaluate the importance of both mechanisms of vicariance in other African rainforest taxa.

Preferential gene loss or retention following genome duplication in allopolyploid species of *Tragopogon* (Asteraceae)?
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After whole genome duplication (WGD), duplicate genes are expected to diverge in function or be lost. Many extant plant lineages show evidence of at least one round of ancient WGD, including model species *Arabidopsis thaliana* and *Oryza sativa*. Previous work in these species identified four protein functional domains which tend to be retained as duplicates ('deletion-resistant' genes), and 23 which tend to be retained as singletons ('duplication-resistant' genes)[Paterson et al. 2006, Trends in Genetics]. We are interested in the regularity and rate at which these genes may reach their fates. We examined patterns of gene loss in three putative 'deletion-resistant' genes and nine putative 'duplication-resistant' genes in the allopolyploid *Tragopogon miscellus*, in five natural populations of independent origin which underwent WGD within the last 80 years (40 generations) and in first-generation synthetic *T. miscellus* plants. We also characterized gene expression in leaf tissue in these populations for seven of the genes. We found apparent loss of genes in natural populations, which, contrary to our expectation, occurred preferentially in the putative 'deletion-resistant' genes. Gene silencing was more frequent than gene loss, and occurred non-significantly more often in the putative 'duplication-resistant' genes. Gene loss and silencing events were apparently repeated in the polyploid populations of separate origin. We did not find gene loss or silencing in the synthetic allopolyploids. This suggests that duplicate gene loss and silencing occur gradually and haphazardly following WGD, perhaps providing variation in gene copy number upon which natural selection can act.

Three potentially functional families of LTR retrotransposons are present in the genome of the choanoflagellate *Monosiga brevicollis*
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The choanoflagellates have long been suspected to be the sister group of Metazoa and interest in this order of nanoflagellates is rapidly increasing. The current draft of the Monosiga brevicollis genome has revealed the presence of three families of LTR (long terminal repeat) retrotransposons, but the apparent absence of non-LTR retrotransposons and transposons. One of the newly discovered families falls in the chromovirus clade of the Ty3/gypsy group and the other two families are closely related members of the Ty1/copia group. EST sequences and nucleotide analyses show that all three families are transcriptionally active and potentially functional within the genome of *M. brevicollis*. We have also discovered seven new families of transposable element that are transcribed within the genomes of five other protist opisthokonts.

Epistatic interactions modify dominance of loci causing hybrid male sterility between *Drosophila persimilis* and *D. pseudoobscura bogotana*

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Understanding the genetic architecture underlying hybrid male sterility requires not only knowledge of the loci causing hybrid problems but also knowledge of the genetic interactions between such loci. Hybrid sterility must result from interactions of sterility alleles of one species with a foreign genome, as these alleles do not cause sterility within species. However, the potential for the modification of dominance via epistasis between sterility-causing alleles has not yet been formally explored. Here, I examine interactions between autosomal loci from *Drosophila persimilis* that cause hybrid male sterility in a *D. pseudoobscura bogotana* genetic background. The results show that the dominance of one locus may influence that of another locus, and suggest that recessive loci localized through previous introgression and mapping studies may potentially contribute to F1 hybrid incompatibilities. The modification of dominance by epistasis may have strong implications for assumptions underlying theoretical models of hybrid incompatibilities.

Components of genetic variance in female fertility in *Drosophila melanogaster* suggest contributions from alleles at intermediate frequencies.

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The number of loci (n) contributing to quantitative trait variability in a random-mating population can be estimated from the dominance variance a random-bred population (VD) and the inbreeding load (B, the regression of the mean trait value on the inbreeding coefficient). Under rather wide conditions, the following inequalities hold: $B^2/V_D = n$ and $V_D/B = B'$, where B' is the mean of the inbreeding load per locus, an indicator of the size of effects of individual loci. This method was implemented for the trait early fecundity of female *Drosophila melanogaster*. A partial diallel cross design was used to estimate the coefficients of additive and dominance variance (CV_A, and CV_D), as well as B, for genes on the third chromosome in lines extracted from a large laboratory population. The overall means and standard errors of these statistics across replicate experiments were 0.071±0.019 and 0.086±0.040, respectively. Using equation (1), together with the mean B value of 0.25±0.029 (relative to the population mean), we obtained an estimate of 8.5 for n, and a B' of 0.030 (relative to the population mean). This suggests that a relatively small number of genes of moderate effect, with alleles at intermediate frequencies, contribute to trait variability, consistent with earlier results from selection experiments.

High DNA sequence diversity in pericentromeric genes of the plant *Arabidopsis lyrata*

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Differences in neutral diversity at different loci can be due to differences in mutation rates or to indirect effects of natural selection acting at closely linked loci (genetic hitch-hiking processes or the effects of balancing selection). Consistent with hitch-hiking models, *Drosophila melanogaster* chromosome regions with very low recombination have unusually low nucleotide diversity. Many plant species, including *Arabidopsis thaliana*, have regions with low crossing-over surrounding the centromeres, yet diversity in pericentromeric region genes of *A. thaliana* is slightly higher than for genes in chromosome arm regions. Because an inbreeding species, such as *A. thaliana*, has low effective recombination, large differences in hitch-hiking are not expected between genome regions. We therefore compared diversity in pericentromere region genes and chromosome arm region genes in *A. lyrata*, an outcrossing close relative. With similar gene densities in the chromosome arms and the pericentromere regions, hitch-hiking effects should be weaker on the chromosome arm genes, in an outcrossing species, because in these regions recombination occurs between heterozygous genotypes; we thus expect higher diversity in arm regions, as in *D. melanogaster*. However, in *A. lyrata*, we found high nucleotide diversity in pericentromeric genes as well as arm region genes. Our data suggest that the gene density in chromosome arm regions is high enough to cause hitch-hiking that reduces diversity to levels similar to those in centromere region genes. Our results suggest that the diversity difference between high and low recombination regions need not always be positive, but will depend on the extent of selection and the gene densities.

Spatio-temporal genetic variability in Spanish Atlantic salmon populations
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Spanish Atlantic salmon (*Salmo salar*) populations have been in decline for much of the last century, with some populations now critically endangered. Small and declining populations are typically expected to lose genetic variability through drift. Our previous research has shown that non-native stocking of four Spanish Atlantic salmon populations had significantly altered mtDNA haplotype frequencies, but the populations had not lost any genetic variability with respect to mtDNA. Here we examine the same populations, using historic scales and more recently collected tissue, at a suite of neutral microsatellite loci. We present the population genetic data that shows that these small populations have not lost nuclear genetic variability despite decline, and that the nuclear microsatellite allelic frequencies have been stable over time.

Ecological modelling and phylogeography of European freshwater snails: can we predict the impact of climate change?
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Changes in biodiversity are likely to happen because of the predicted global climate warming that will alter abiotic conditions on large spatial scales. While some of the emerging conditions may be buffered by phenotypic plasticity and/or local adaptation, significant changes in species ranges may be expected. We present here an approach to infer niche conservatism of freshwater snails (Pulmonata). This evaluation provides useful insights on the impact of climate change on the geographical ranges of two Pulmonates species, Ancylus fluviatilis and Radix sp. First, we performed a range-wide sampling of the species and subjected it to phylogenetic and phylogeographical analyses of mitochondrial DNA (COI and 16S). Nested clade analyses were performed to elucidate the species evolutionary history, and gave us an insight of the refugial areas and the events that lead to the current patterns. Second, we analysed the climatic niche of both species. The niche requirements of A. fluviatilis vary in space; the phylogroups inferred from the phylogeographic analysis occupy distinct niches. The niche evolution inferred for A. fluviatilis adds thus a cautionary note to the use of climate niche modelling in this species. Ecological Niche Modelling allowed us to project the current ecological requirements of Radix onto climate surfaces for the Last Glacial Maximum. The suitable area modelled matches the results of the phylogeographic analyse. Niche conservatism occurs in Radix. This result allows thus the prediction of this species range in the context of global warming.

Population consequences of environmental sex reversal
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When sex determination is predominantly genetic but environmentally reversible, exposure to exogenous hormone-active substances can lead to population sex ratio changes and a frequent mismatch of gender phenotypes and genotypes. Such scenarios may be becoming increasingly common in many fish and amphibia, yet their effects remain largely unexplored from both theoretical and empirical perspectives. Here I evaluate the consequences for natural populations of exposure to estrogenic or androgenic substances that are present in many effluents of industrial and domestic origin. Similar findings are expected for other environmental factors, such as changes in global or local temperatures. My results suggest that environmental sex reversal affects population growth and sex ratios in some counter-intuitive ways, and can change sex determination from predominantly genetic to fully environmental, often within only a few tens of generations. Populations that have lost their genetic sex determination may then quickly go extinct if the environmental sex reversal ceases.

How to test a biologically meaningful null hypothesis of no linkage disequilibrium in finite population samples?

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We demonstrate that the commonly tested null hypothesis of zero linkage disequilibrium (LD) is a statistically convenient, but biologically irrelevant null hypothesis. This is because the null hypothesis of zero LD can only be true in an infinitely large population. In finite populations, small but non-zero amounts of "background LD" are always present. Thus, the biologically meaningful null hypothesis is that of free recombination in a finite population. This null hypothesis, however, is extremely difficult to test. We therefore suggest an approximate testing procedure. Our new procedure highlights that it is impossible to draw inferences about linkage from LD data alone but additional information about N_e and the mutation rate and model is required. Our simulations suggest that while testing the statistically convenient null hypothesis will lead to alarmingly high false positive rates, with our new testing procedure, mis-inference can be avoided. We demonstrate the use of our new testing procedure on a real data set of red deer and also highlight the limitations of our method.

Can Pleistocene refugia explain current Neotropical biodiversity

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There are a number of competing hypotheses seeking to explain the high species diversity found in the Amazon. According to the refugium hypothesis, drier conditions during the Pleistocene led to allopatric speciation in forest refuges. A consequence of such a mode of diversification is that divergence times between pairs of sister taxa will be clustered and not scattered in time. Focusing on a “suture zone” (zone of correlated hybrid and contact zones between sister taxa) between lowland Amazonian and highland Andean Heliconiine and Ithomiine fauna in eastern Peru, we have obtained mtDNA and multiple nuclear gene sequences for over 20 pairs of sister taxa. Using an MCMC coalescent approach we obtain species divergence time estimates to test the refugium hypothesis.

Distribution is a poor predictor of infraspecific genetic variation in *Androsace* sect. *Aretia*

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Chorology, the study of distributional areas of species and other taxa, has a long history, and has been used to categorise species into broad classes of distributional types. Some apparently relict distributions are seen as evidence of previously wider distributions, while widespread, continuous distributions may be seen as indicative of more recent range expansion. In *Androsace* sect. *Aretia* (*Primulaceae*), a group of 20 or so species mostly restricted to the European Alpine System, distributional areas are found to have little predictive power concerning the amounts and patterns of infraspecific genetic variation. Against expectations, some species, such as *A. hausmannii* and *A. halleri* which have disjunct distributions and inhabit possible glacial refugia are found to be invariant, while species such as *A. alpina* or *A. pubescens* harbour considerable genetic variation within continuous distribution areas. This demonstrates that, because different demographic processes can lead to the same distributions, the history of a species cannot be reliably predicted from its area of distribution alone.

Variability in disease prevalence stabilises host-parasite coevolution by generating density-dependent selection

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It has been shown that to maintain observed polymorphisms at plant and pathogen gene-for-gene (immune recognition) loci, one or both of the alleles involved must experience negative frequency-dependent selection such that as an allele grows more common selection for it decreases. Models investigating gene-for-gene dynamics often ignore epidemiological factors and assume disease prevalence (the proportion of a given population exposed to a disease) is total. However, disease incidence actually varies greatly in both agricultural and wild plant-pathogen associations. Here I discuss two models simulating less than total disease incidence. The first is a single-patch model where incidence changes over time. The second uses two patches linked by gene-flow, where incidence is fixed but different in each patch. Both models can lead to stable polymorphism at resistance loci in plants and avirulence loci in animals.

Speciation out of the Andes: patterns of diversification of neotropical ithomiine butterflies

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The Neotropics harbour highly diverse ecosystems, but the causes underlying the origins and maintenance of such diversity are still poorly understood. Dated species-level phylogenies enable testing some commonly invoked hypotheses, such as the role of Pleistocene refugia or the uplift of the Andes. Here we use ithomiine butterflies (Nymphalidae: Ithomiinae) as a model. The Ithomiines are a diverse subfamily of exclusively neotropical butterflies. They are involved in mimetic interactions with other butterflies, and dominate butterfly communities. We generated a species-complete molecular phylogeny for the genus Napeogenes (24 species) and used a published phylogeny of the genus Ithomia (23 out of the 24 species) to infer the patterns of diversification of both genera through time. Both genera started diversifying about 8-15 Mya, when the Andes were already present. Early diversification rates were high, with most of the lineages already present before the Pleistocene, thus ruling out the prevalence of recent refugia to account for speciation in these genera. Analysis of the elevation range of extant taxa and maximum likelihood reconstruction of ancestral states indicate that both genera originated in altitude. Both genera diversified gradually down the Andes, with most of the youngest species occurring at low elevations. Recolonisations of higher elevations were rare. Unlike previous findings in birds and other butterflies, here the Andes may not have acted as a “pump” for new species, but rather as a “reservoir” of older species, which then diversified by colonising lower elevations. We discuss additional factors that may have promoted diversification within elevation level, such as ecological speciation driven by mimicry.

Ancient DNA and the time dependency of mutation rates

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The increasing ability to extract and sequence DNA from non-contemporaneous tissue offers biologists the opportunity to analyse ancient DNA (aDNA) together with modern DNA (mDNA) to address the taxonomy of extinct species, evolutionary origins, historical phylogeography and biogeography. Perhaps more exciting are recent developments in Bayesian MCMC integration that offer the potential to use temporal information from aDNA and mDNA for the estimation of mutation rates and divergence dates. This comes at a time of growing interest in the possibility of time dependency for molecular mutation rate estimates, offering an alternative to fossil and geological calibration for the estimation of mutation rate. Here I review the evidence for time dependent mutation rates, with particular reference to estimates from aDNA.

The degeneration of Y chromosomes through Muller's ratchet: A simulation study
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A typical pattern in sex chromosome evolution is that Y chromosomes have lost many of their genes. One mechanism that might explain this degeneration is Muller's ratchet, the recurrent stochastic loss of Y chromosomes carrying the fewest number of deleterious mutations. present simulation results of a model in which lethal recessive mutations arise on both X and Y chromosomes. These results demonstrate that Muller's ratchet can be slowed down considerably by the presence of mutations on the X chromosome. On the other hand, a lower mutation rate in females than in males, background selection and dosage compensation can accelerate the process.

X vs autosomal comparison of DNA polymorphism in *Silene latifolia*
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Theory predicts that the lack of recombination on the Y chromosome should result in a substantial reduction of genetic diversity in Y-linked genes due to processes such as background selection and selective sweeps. It was previously demonstrated that DNA diversity in the *S. latifolia* Y chromosome is indeed drastically lower than in the X-linked genes. However, the comparisons with other genomic compartments are still missing. Here we report comparisons of DNA polymorphism in five pairs of S. latifolia sex-linked genes and 20 unlinked autosomal loci. Surprisingly, the autosomal loci in *S. latifolia* are less polymorphic, compared to X-linked loci, which is contrary to what is expected from their ploidy. Thus, previous comparisons of the level of polymorphism on the *S. latifolia* X and Y chromosomes may have overestimated the reduction of DNA diversity for the Y chromosome in this species. The reasons for the higher DNA diversity in the X chromosome, compared to autosomes and implications of this finding to our understanding of Y chromosome evolution are discussed.

Temperate forest refugia and postglacial expansion in Europe: the eastern story.
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Previous genetic evidence indicates that during the last glacial maximum (LGM) temperate forest species were restricted to refugia in the Italian, Iberian and Balkan peninsulas. However, recent palaeontological data have been interpreted as supporting the existence of more northerly refugia, which would subsequently have had a significant effect on the distribution of extant genetic diversity. In order to understand the role of glacial refugia in shaping the genetic diversity of extant temperate forests, we have carried out a detailed investigation of the chloroplast DNA diversity of temperate tree species within the Balkan peninsula and neighbouring areas. We investigated species with contrasting life history traits: five species of white oaks, dominant species in many European forests with high dispersal ability, and hornbeam, a poorly dispersing hardwood species whose distribution has changed dramatically in different interglacial periods. By using a population-level sampling approach applied across a very broad geographic range and exploiting the greater resolution offered by sequencing (>5kb per individual), we have located glacial refugia for these species and have inferred the history of their post-glacial expansion. The distinctive phylogeographic patterns observed are highly consistent with palaeo-climatic predictions, yield insights into the northern versus southern refugia debate, and demonstrate how life history, topography and climate change interact in shaping extant patterns of genetic diversity.

Endosymbiont infections and dispersal strategy of the money spider *Erigone atra*

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Dispersal plays a key role in shaping biological and ecological processes such as the distribution, dynamics and viability of spatially-structured populations and species, or the pace and scale of invasion. We show here that vertically transmitted, bacterial endosymbionts of the Rickettsia group are a significant factor determining dispersal strategy of an important pest-controlling spider. Infection is associated with decreased tendency for long-distance dispersal, which potentially increases genetic isolation within the wider meta-population through reducing gene flow. The result is of general importance given the widespread occurrence of similar endosymbionts in arthropod communities.

Selection, sequences, phenotypes, and fitness in an intertidal snail

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If we can identify those DNA sequences which are evidently under selection in wild populations, characterise these sequences, and find evidence of associated fitness effects, we are making progress in understanding the operation of selection at the 'genomic' level. Here we describe such a sequence in an intertidal snail (*Littorina saxatilis*), showing that its variation is evidently related to shell form and variation in female fecundity.

The colonisation of Ireland: myths, mystery, and molluscs

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While more than 99% of the Irish biota is in common with Britain, it has long been recognised that there is also a characteristic but mysterious "Lusitanian" element, since several species are present in Iberia and Ireland but absent from Britain (e.g. Strawberry tree, Kerry slug). Although the land snail *Cepaea nemoralis* is widespread across Europe, it has been suspected that some populations on the west coast of Ireland may have a Spanish, specifically Pyrenean, origin because of their characteristic morphology. I therefore obtained molecular sequence data for this species, using snails from over 102 separate locations across Western Europe, including a transect across the North of Spain and the Pyrenees, and collected mitochondrial sequence data for >850 individuals. Phylogenetic analysis of these sequences reveals that the majority of Irish populations probably originate from a geographically restricted source in the Pyrenees, supporting similar recent results in other species. Given that fossil data indicates the presence of *C. nemoralis* in Ireland for at least 8000 years, the significance of these findings in relation to the post-glacial colonisation of Ireland will be discussed. One immediate consequence is to wonder how many other Irish species are of cryptic "Lusitanian" or Iberian origin?

'Porous' species boundary between *Silene latifolia* and *S. dioica*.
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Silene latifolia (white campion) and *Silene dioica* (red campion) are two closely related dioecious species with ranges that broadly overlap across Europe. In geographical areas where the two species coexist, hybridization may be possible, leading to gene flow between these two phenotypically distinct species. Previously it was demonstrated that although interspecific gene flow is observed for two X-linked genes, there is almost a total absence of gene flow for Y-linked genes, suggesting that interspecific introgression of the Y chromosome is prevented by selection. Alternatively it may be the X-linked genes that are "unusual" in their ability to cross the species boundary. To establish the genome-wide rate of gene flow between the two species, we studied DNA diversity in 19 autosomal loci in a sample of 15 individuals from each species. Most autosomal loci show less differentiation between the species (Average Fst=0.39), compared to Y-linked genes. However, in some instances, autosomal loci demonstrated strong differentiation with no evidence of gene flow between the two species (Fst=0.95). Monte Carlo Markov Chain modeling indicated low levels of gene flow, possibly skewed in the direction of *S.latifolia* to *S.dioica*. Similarly, Structure analysis revealed split membership of some individuals to the two species clusters, particularly in the S.dioica individuals. Thus, *S.latifolia* and *S.dioica* may conform to the "porous species boundary" model of speciation, with some genes freely flowing between the two species, while a fraction of the genome (including the Y chromosome) is unable to cross the species boundary, possibly because they are disadvantageous in the alien genetic or ecological environment.

Evolution in the fast lane: tales from male-killer/host interactions in the South Pacific
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Male-killing bacteria are found in a many insects, and theory indicates they produce strong selection on their host to prevent their action or transmission. We present data on the dynamics of this interaction from field populations, and show rapid spread of host suppressor genes-representing one of the fastest cases of natural selection recorded in the wild.

Gene expression variation in African and European populations of *Drosophila melanogaster*
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Changes in levels of gene expression can have large consequences for the phenotype of an organism. Variation of gene expression in natural populations might therefore serve as a substrate for positive Darwinian selection, and hence play a role in the adaptation of populations to their local habitats. We profiled the genome-wide expression of adult males of 16 *Drosophila melanogaster* lines. The flies come from two natural populations with vastly different environments, Zimbabwe and the Netherlands. Our approach allowed us to estimate the levels of gene expression variation within each population and detect genes that show expression patterns which differ significantly between the two populations and hence are candidates for local adaptation. We find that variation is equal in both populations. This argues for stabilizing selection as the major force shaping expression polymorphism. Supporting this view, genes that are under increased selective constraint, because they are involved in many different biological processes, tend to be less variable. We observe that there is substantial population differentiation at the gene expression level. Candidates to have undergone adaptive evolution in Europe include genes that are putatively involved in insecticide resistance. Surprisingly, many genes overexpressed in Africa play a role in the formation and function of the flying apparatus.

CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure

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Clustering of individuals into populations on the basis of multilocus genotypes is informative in a variety of settings. In population-genetic clustering algorithms, such as BAPS, STRUCTURE and TESS, individual multilocus genotypes are partitioned over a set of clusters, often using unsupervised approaches that involve stochastic simulation. As a result, replicate cluster analyses of the same data may produce several distinct solutions for estimated cluster membership coefficients, even though the same initial conditions were used. Major differences among clustering solutions have two main sources: (1) 'label switching' of clusters across replicates, caused by the arbitrary way in which clusters in an unsupervised analysis are labeled, and (2) 'genuine multimodality,' truly distinct solutions across replicates. To facilitate the interpretation of population-genetic clustering results, we describe three algorithms for aligning multiple replicate analyses of the same data set. We have implemented these algorithms in the computer program CLUMPP (CLUster Matching and Permutation Program).

Comparative *Plasmodium* genomics and population genomics of the malaria parasite *Plasmodium falciparum*.

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The malaria parasite *Plasmodium falciparum* is an extremely prevalent parasite that claims the lives of more children worldwide than any other infectious disease. We are using both genome-wide genetic diversity data and comparative analysis of *Plasmodium* genomes to understand more about functional elements of the genome and their evolution. Our initial genomic scale studies of genetic diversity with low-coverage comparisons of three isolates and the chimpanzee parasite *Plasmodium reichenowi* (Jeffares et al. 2007) indicated that intergenic regions were slightly less polymorphic than exons (exon $\pi = 1.27 \times 10^{-3}$, intergenic $\pi = 1.21 \times 10^{-3}$), suggesting strong functional constraints in intergenic regions. The divergence between *P. falciparum* and the chimpanzee parasite *Plasmodium reichenowi* showed the same pattern (exon d = 20.2 $\times 10^{-3}$, intergenic d = 23.6 $\times 10^{-3}$), and indicated that intron regions were constrained relative to fourfold degenerate and synonymous sites (intron d = 26 $\times 10^{-3}$, four-fold degenerate sites d = 55 $\times 10^{-3}$, synonymous sites d = 71 $\times 10^{-3}$). More detailed (unpublished) analysis of divergence between *P. falciparum* and *Plasmodium reichenowi* indicated that introns were particularly conserved within ~ 5nt from exons, and that intergenic regions less divergent between 800 -1500 nt from adjacent genes. These analyses indicate that many functional elements remain to be characterised. To that end we are conducting new analysis with A) more genome-wide polymorphism data (from 5 isolates at about 8x coverage), and B) exon-synteny anchored whole genome alignments of six species (primate parasites *P. falciparum*, *P. vivax*, *P. knowlesi*, and rodent parasites *P. berghei*, *P. yoelii yoelii*, *P. chabaudi*). While genomes are relatively few and in draft form, phylogenetic distances within primate species alone should be sufficient to discover many new functional units (eg: median *P. falciparum - P. vivax* divergence exons = 0.47, intergenic = 0.61). We will present an analysis of conserved non-genic (intergenic and intronic) regions in *Plasmodium* genomes. Our initial analysis indicates that there are many highly conserved non-genic regions in these genomes. For example using *P. vivax - P. knowlesi* pairwise divergence we find 350 intergenic regions (100nt length) that are less divergent than 95% of exonic regions.

Evolution of a genome defence system

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Repeat-induced point mutation (RIP) is a mechanism by which many fungi destroy and diversify transposable elements in their genomes, reducing the risks of insertional mutation and ectopic recombination. We sample populations of copia-like retrotransposable element elements from within the genomes of ten strains of anther-smut fungus (*Microbotyrum violaceum* species complex) and investigate the efficacy of RIP as a genome defence.

Towards the identification of a butterfly colour-pattern supergene

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Heliconiine butterflies are well knwon for the diversity of their mimetic colour patterns, which is under the relatively simple genetic control involving few large effect Mendelian loci. At the pinnacle of this simplified genetic architecure, the polymorphic mimicry of *Heliconius numata* is controlled by a single supergene which switches between wing patterns themes that are nearly exact mimics of co-occurring *Melinaea ithomiines*. In contrast, the geographic diversity of the co-mimics *H. erato* and *H. melpomene* is controlled in both species by a "toolkit" of major loci on several different chromosomes. I have showed that the *H. numata* supergene is positionally homologous to one of the toolkit loci in *H. melpomene* and *H. erato*, showing that convergent and divergent phenotypes are controlled in part by homologous, flexible loci. I will here show new results of the fine mapping of the *H. numata* supergene P and other *Heliconius* colour pattern toolkit loci to discuss the evolution of the genetic architecture of mimicry. I will then present new population genetics results showing how association studies from wild polymorphic populations can allow for the identification of the genes involved in adaptive diversity in *Heliconius* butterflies.

Hill-Robertson interference among strongly selected sites reduces their effects on linked neutral sites.

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Under tight linkage, evolution at any one site is not independent of evolution at other sites, leading to a reduction in effective population size, Ne. There is, however, a discrepancy between the observed levels of nucleotide diversity and those predicted under the background selection model: with many linked sites under selection, the reduction in Ne is consistently overestimated. To investigate if Hill-Robertson interference among strongly selected sites undermines the effects of background selection, computer simulations were carried out using parameters of mutation, selection and recombination, appropriate for deleterious amino-acid mutations in *Drosophila melanogaster* populations. The results show that, indeed, the background selection model needs to be modified to accurately describe the reduction in neutral diversity caused by many linked sites under strong selection, and suggests that this effect may reach a plateau when many such sites are closely linked.

Parallel length expansions in the thioredoxin h1 protein during an adaptive radiation in the Hawaiian plant genus *Schiedea* (*Caryophyllaceae*).

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Explosive" island adaptive radiations are accompanied by tremendous phenotypical and ecological changes suggesting strong positive selection. However, our knowledge of molecular mechanisms behind such events is quite patchy. Expansions and contractions of amino acid repeats in proteins which might be implicated in "explosive" radiations are commonly neglected by researchers. To evaluate a role of amino acid repeats polymorphism during adaptive radiations we analysed thirty protein coding genes in 27 species of *Schiedea*, which is one of the largest plant radiations on the Hawaiian Islands. One of the analysed genes, TRX-H1, possessed a remarkable length polymorphism in the terminal exon. The TRX-H1 gene encodes thioredoxin h1, which is specific to plants and involved in protection against oxidative stress and carbon/nitrogen metabolism regulation. Polythreonine repeats up to sixteen amino acids in length occur at two loci of the protein C-terminus and their distribution is incongruent with Schiedea species phylogeny. Given that similar patterns of polythreonine repeats were found in phylogenetically distant parapatric species it is likely that the thioredoxin h1 length polymorphism has been created not by drift but instead by positive selection. Importance of structural differences in the C-terminal helix have been shown by comparing crystallized structures of Arabidopsis and poplar h1 thioredoxins, while no major changes in the active site conformation have been observed (Peterson et al. 2005). Our findings add to already known cases suggesting that repetitive amino acid motifs might provide a mechanism for rapid morphological and ecological evolution (e.g. Lindqvist et al. 2007).

The frequency of rDNA variants within individuals provides evidence of population history and gene flow across a grasshopper hybrid zone

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In the grasshopper *Podisma pedestris*, units of the ribosomal DNA (rDNA) multigene family are not identical, but comprise multiple genetic variants. We surveyed this variation using a novel pyrosequencing approach. The colonisation history of the study area is well know as it can be inferred from the distribution of two chromosomal races which invaded from different directions after the last glacial maximum and finally met to form a hybrid zone. The rDNA data showed additional genetic substructure within the chromosomal races indicating previously unsuspected routes of postglacial colonisation. The two races were found to have genetically distinctive rDNA composition, which suggests that variation can persist for thousands of generations. These differences can be exploited in the hybrid zone to investigate the potential involvement of rDNA sequence polymorphisms in genomic incompatibilities between the two races. We found that the association between chromosomal race and rDNA composition has been broken down within the zone. It therefore appears that rDNA variants move freely across the zone and are not under opposing selection pressures in the two races.

Phylogeography of Eurasian *Larix* species inferred from nucleotide variation in two nuclear genes

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Larch (*Larix* Mill.) is one of the most widely distributed tree genera in Eurasia. To determine population structure and to verify classification of five species and three varieties of the Eurasian *Larix* species, we investigated levels and patterns of nucleotide variation of two nuclear gene regions: the 4-coumarate coenzyme A ligase (4CL) and the coumarate 3- hydroxylase (C3H). In the 4CL region nucleotide diversity at silent sites varied between 0.0020 in *L. gmelinii* to 0.0116 in *L. gmelinii* var. *japonica* and in the C3H region between 0.0019 in *L. kaempferi* to 0.0066 in *L. gmelinii* var. *japonica*. In both gene regions statistically significant population differentiation (F_{ST}) was detected among adjacent refugial populations of some species suggesting limited gene flow and/or long time isolation of some refugial populations. On the other hand, populations of *L. sukaczewii* from northwestern Russia, which was glaciated 20,000 years ago showed no differentiation. This result is consistent with recent postglacial origin of these populations. Haplotype composition of some of the investigated Eurasian *Larix* species suggested that they are considerably diverged. Some haplotypes were unique to individual species. Our results indicate that more intensive sampling especially from known refugial regions is necessary for inferring correct classification of Eurasian *Larix* species and inferring their postglacial migration.

MHC variability in a unisexual vertebrate

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Poecilia formosa is a small live-bearing fish that inhabits fresh water streams of northern Mexico and southern Texas. It was the first vertebrate discovered to reproduce clonally and as all unisexual vertebrates it is a hybrid species. Different ploidy levels are found within the species all of which reproduce gynogenetically. We have been interested in the question whether a third set of chromosomes may provide an advantage for the clonal species e.g. by adding additional genetic variability and buffering the organism against the accumulation of deleterious mutations. So far, however, we only found negative effects of triploidy: triploids reproduce slower (Lamatsch et al. unpublished) and show a lower genotypic variability in field populations of *P. formosa*. We are now investigating the question whether the variability of certain genes might be more important for fitness than the overall genetic variability as detected by microsatellites. MHC genes play an important role in vertebrate immune function and variability seems to be a key factor in their effectiveness. We look at MHC variability in *P. formosa* at different ploidy levels and also compare the MHC variability found in this clonal species with the MHC variability found in its sexual parental species. Our results show that diploid *P. formosa* are not as variable as their parental species. Surprisingly, triploids seem even less variable than diploids.

Effect of balancing selection on spatial genetic structure within continuous populations: theory and empirical evidence from the self-incompatibility locus in *Arabidopsis halleri*

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Within plant populations, as pollen and seed dispersal are commonly spatially restricted, genetic similarity among individuals is higher among neighbouring than among more distant individuals. This pattern of isolation by distance is influenced by mating systems, like selfing avoidance which reduces the spatial genetic structure (SGS). The SGS could also be influenced by the effect of natural selection, like strong balancing selection acting on self-incompatibility systems. By numerical simulations, we investigated the SGS within populations at neutral loci and the self-incompatibility locus (S-locus) under different conditions of seed and pollen dispersal, immigration rate and allelic diversity at the S-locus. In some circumstances, we found a significantly lower extent of SGS at the S-locus than at neutral markers, whatever the self-incompatibility system considered. In analogy to previous theoretical results on population structure at self-incompatibility genes, we interpreted these results as evidence for a higher effective dispersal of alleles at the S-locus as compared to neutral loci. We also investigated the SGS for the S-locus and for 11 microsatellite markers in three natural populations of *Arabidopsis halleri*, a species with sporophytic self-incompatibility. The observed patterns of SGS were highly variable, a result that we interpret because of different ecological and demographical conditions encountered in the three studied populations.

The distribution of mutational effects on fitness within genes

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Advances in methods for estimating the distribution of mutational effects on fitness have recently led to remarkable insights into important features of this distribution when mutations occur randomly throughout the whole genome. This distribution is fundamental for quantifying many problems in evolutionary biology and systems biology. Here we present a method for estimating the expected width of a distribution of deleterious mutational effects within genes from a sample of DNA sequence diversity values. We apply our new method to sequences from Drosophila melanogaster. Building on earlier results that found the lognormal distribution to be particularly useful (Loewe & Charlesworth, Biology Letters 2(2006)426-430), we find that most of the variability of selection coefficients between sites in a genome is also expected between sites within typical genes. This means that most genes are expected to have non-synonymous mutations with hugely different effects, ranging over many orders of magnitude from effectively neutral to strongly selected.

How to measure starshape in genealogies? Summary statistics and demographic inference

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Tajima's D and related measures are widely used to test for departures from the standard neutral model. However, such neutrality tests are far from ideal, given that they are affected by the topological balance of the underlying genealogy, which is unaltered by changes in effective population size. Some simple statistics, which consider the degree of starshape of a rooted genealogy, are proposed. An exponential model of population growth and coalescent simulations are used to compare the power of these statistics to classical neutrality tests and likelihood methods for the single and multi-locus case. These measures of starshape are more powerful and require smaller sample sizes than standard tests of neutrality and may be a useful alternative to full likelihood estimation given reliable outgroup information.

Genetic diversity in relation to ploidy and mating system in *Arabidopsis lyrata*
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Arabidopsis lyrata is increasingly being used as a model for plant population biology because it is one of the closest outcrossing relatives of the more widely used but highly selfing model *Arabidopsis thaliana*. The "species" currently includes three (or possibly four) subspecies, defined largely based on geographic distribution. However, not all populations are outcrossing, not all populations are diploid, and hybridization likely occurs with other closely related species in at least some regions. When using this plant as a model, it is thus important to take into account variation in population structure, mating system, ploidy and potential for introgression in plants sampled from different geographic regions. We have been using microsatellite markers and gene families involved in controlling the mating system to investigate how such factors influence genetic diversity in populations of *A. lyrata* sampled from eastern North America, Alaska, Europe, and Japan. Results will be discussed in terms of the utility of these markers for resolving questions about origins of polyploids and inferring inbreeding in diploids.

The evolutionary rate of multigene families under concerted evolution
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The evolution rate of a gene is the substitution rate, whichis a product of the mutation rate and the fixation probability. As is well known, the fixation probability under genic selection is [1-exp(-4Nsp)]/[1-exp(-4Ns)], where N is the effective population size and s,p are the selection coefficient and the initial frequency of the mutant. The fixation within a multigene family under concerted evolution is a phenomenon that a mutant spreads across all member of the multigene family. We considered the fixation probability via gene conversion by using diffusion model and computer simulation. It was suggested that the probability is given only by the selection coefficient and the initial frequency: [1-exp(-n4Nsp)]/[1-exp(-n4Ns)], where n is the number of loci and p is the arithmetic mean of the initial frequencies of the mutant at all loci. Under selection with dominance, there was no simple result like this.

Characterising MHC variation in the endangered African wild dog (*Lycaon pictus*).
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Loss of adaptive variation arising from population declines and fragmentation is a primary concern in conservation. However, direct assessment of adaptive variation has been hampered by a lack of knowledge about the underlying genetic causes. The Major Histocompatability Complex (MHC) is a group of genes known to be important in effective immune responses. As one of the best understood set of adaptive genes, the MHC can provide a proxy for adaptive variation. African wild dogs have suffered extensive declines and now persist as small and fragmented populations totalling less than 5,000 individuals. Recurrent disease epidemics pose a significant threat to this species, therefore knowledge of MHC variation is particularly pertinent for conservation. In this study, we assessed variation at three MHC Class II genes (DRB, DQB, DQA) in free ranging populations in Eastern and Southern Africa as well the European captive zoo population. Our MHC data show patterns of variation that are indicative of historical loss of variation, followed by more recent diversification. Furthermore, we find differences in the distribution of allele variation between loci from that of other canids. Additional analyses of a mitochondrial D-Loop fragment have highlighted important differences in the population structure of MHC alleles and mtDNA haplotypes.

Pathogen evolution and disease emergence in carnivores

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Emerging infectious diseases (EIDs) constitute some of the most pressing problems for both human and domestic animal health, and biodiversity conservation. It is not clear if the removal of past constraints on geographic distribution and transmission possibilities for pathogens alone are sufficient to give rise to novel host-pathogen combinations, or whether pathogen evolution is also generally required for establishment in novel hosts. Previ ous studies of genetic sequences have given insights into the evolutionary pressures acting on populations of a number of important pathogens, and detected that specific genes and specific residues are under the influence of positive selection. However, few of these studies have been able to associate specific substitutions with changes in virulence or host specificity. Canine distemper virus (CDV) is a morbillivirus that is prevalent in the world dog population, and poses an important conservation threat to a diverse range of carnivores. We performed an extensive phylogenetic and molecular evolution analysis on complete sequences of all CDV genes to assess the role of selection and recombination in shaping viral genetic diversity and driving the emergence of CDV in non-dog hosts. We tested the specific hypothesis that molecular adaptation at known receptor binding sites of the hemagglutinin gene is associated with independent instances of the spread of CDV to novel non-dog hosts in the wild. This hypothesis was upheld providing compelling evidence that repeated evolution at known functional sites (in this case residues 530 and 549 of the hemagglutinin molecule) is associated with multiple independent occurrences of disease emergence in a range of novel host species. We have detected interspecies variation within the CDV receptor, signalling lymphocyte activation molecule (SLAM), between carnivore species allowing hypothesis to be drawn regarding the importance of SLAM receptor variants in determining carnivore species susceptibility.

Population expansions in Australian estuarine Glassfish *Ambassis marianus* (Günther 1880) and *Ambassis jacksoniensis* (Macleay 1881)

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Through the use of mitochondrial DNA (ATP8 gene), phylogeographic patterns were investigated in two species of estuarine Glassfish (*Ambassis marianus* and *Ambassis jacksoniensis*) (Perciformes: Ambassidae) along the coast of eastern Australia. Individuals were collected from estuaries between Tin Can Bay (Queensland) in the north and Kempsey (New South Wales) in the south. Analysis of the haplotype frequencies found in this region suggested panmictic populations with extremely high levels of genetic diversity, but with no correlation between geographic distance and genetic distance. Non-significant F_{ST} and ? $_{ST}$ suggested extensive dispersal among estuaries. However, Tajima's D and Fu's F_S values suggest 'mutation – genetic drift equilibrium' has not been reached, and that population expansions occurring 262000 (*A. marianus*) and 300000 (*A. jacksoniensis*) years ago may obscure any phylogeographic structuring or isolation by distance. The finding of panmixia was contrary to the prediction of genetic structuring intermediate between that of marine fish (shallowly structured) and freshwater fish (highly structured), suggesting high dispersal capabilities in these species.

Molecular phylogenetics and biogeography of the Neocellia series of Anopheles mosquitoes across Southeast Asia

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Southeast Asia is unique amongst tropical regions with regard to the dramatic influence of Pliocene and Pleistocene sea level fluctuations on its biogeography, specifically its landmass configuration, aridity and habitat cover. The likely influences of such substantial environmental changes on population divergence and speciation across Southeast Asia, a global hotspot region in terms of biodiversity, were inferred through the examination of a molecular phylogeny of the Neocellia series of Anopheles mosquitoes. Phylogenetic relationships between lineages were inferred using both mitochondrial and ribosomal DNA. The relative importance of alternative modes of speciation, including allopatric speciation driven by habitat fragmentation, ecological speciation and altitudinal replacement, in generating diversity was investigated. Using a fixed molecular clock and Bayesian MCMC analysis, the majority of speciation events were dated to the late Pliocene, a period characterised by rapid cooling and a dramatic decrease in aridity across Southeast Asia. We suggest that the fragmentation and contraction of suitable habitat during this period, together with differential ecological adaptation within isolated populations, may have driven divergence and speciation events within the Neocellia series. Divergent geographical lineages were detected within several species, and it is suggested that population divergence may have resulted from habitat fragmentation during the Pleistocene glaciations. The widespread distributions of most species across Southeast Asia suggests that populations were able to expand and re-colonise areas following the extension of favourable habitat. Sri Lanka, North East India and Northern Myanmar were identified as possible glacial refugial areas for Anopheles species. The mitochondrial data failed to support the monophyly of the Neocellia series, suggesting that the classification of this series may require revision.

'Mongrel dog' model of speciation and its implication for analysis of sympatric morphs

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Sympatric morph complexes are common among fish faunas inhabiting large lakes. Prominent differences in morphology have been used as basis for description of morphs as species. However, large degree of shared polymorphism at nuclear and mtDNA and observed natural hybridization between morphs often cast doubt on taxonomic status of such morphs and lead to rejection of species status.

I propose a "mongrel dog" model to explain genetic structure of young sympatric complexes. The model is based on an assumption of unidirectional gene flow from derived and specialized morph toward the ancestral generalist, similar to gene flow from "pure-breeds" toward mongrel dogs and not in the opposite direction. Existence of specialized morphs is maintained by the presence of vacant niches, not suitable for generalists, and development of assortative mating system for each morph. This model illustrated by two examples of coexisting fish morphs – large barbs from *Barbus intermedius* complex in the lake Tana (Ethiopia) and Russian/Persian forms of sturgeon in the Caspian Sea.

Lake Tana is a young lake in the upper flow of the Blue Nile and posses a spectacular fish fauna, consisted of 12-15 morphs or species of large African barbs from *B. intermedius* species flock. Different forms have very diverse trophic specialization, and some morphs feeds preferably on plants, mollusks, insects, or small fishes. Shape of head, eye size, pharyngeal tooth armament and length of intestine is considerably different among the morphs. To reveal the degree of genetic segregation among *Barbus* morphs in lake Tana, we sequenced partial D-loop and complete CytB genes (total 1800 b.p.) in 205 specimens of three morphs: most common ancestor-like form *B. intermedius*, and two highly specialized morphs – *B. acutirostris* ("acute" or "long-snout") and *B. macrocephalus* ("big-eye"). As an outgroup, specimens of *B. intermedius* from six different rivers of Blue Nile and Genale river basins have also been sequenced.

MtDNA genealogy approach revealed that *B. intermedius* consisted of very diverse network of mtDNA haplotypes, which reflects large population size and long coalescence time for this ancestral form. On the contrary, *B. acutirostris* presented by few haplotypes, aggregated in several closely related clusters. Thirty seven out of 54 "acute" fish posses haplotype H13, and many other haplotypes in this form are different from H13 by one or two substitutions and are unique for this form. Similar, but more diverse haplotype network was observed in the "Big-eye" morph. This data indicate that specialized morphs in lake Tana are reproductively isolated from the ancestral form.

Persian sturgeon *Acipenser persicus* (Borodin 1897) in the Caspian Sea can be distinguished from sympatric Russian sturgeon (*A. gueldenstaedtii* Brandt & Ratzeburg, 1833) by body coloration and number of meristic characters. However, lack of clear diagnostic morphological characters, occurrence of specimens with intermediate morphology interpreted as a hybrids, as well as inability to distinguish this species by both mitochondrial and nuclear DNA markers, were a ground for serious doubts about validity of *A persicus* as a species. Study of control region mtDNA variation reveals that A. persicus haplotypes form a few tight clusters scattered within wide haplotypes network of *A. gueldenstaedtii*. Lack of gene flow from ancestral *A. gueldenstaedtii* toward *A. persicus* supported by distribution of "baerii-like" haplotypes in the Caspian Sea. Postglacial invasion of Siberian sturgeon *A. baerii* into the Caspian Sea and subsequent intergradation with *A. gueldenstaedtii* and not with *A. persicus* reveal the direction of gene flow between the two native Caspian species. While *baerii*-like haplotype has frequency up to 30 % in Caspian population of *A. gueldenstaedtii*, no one haplotype was observed in all out of 150 studied specimens of *A. persicus*. This is strong evidence, that there is no gene flow from *A. gueldenstaedtii* toward *A. persicus.*

Evolution of the Achaete-Scute Complex in insects: recurrent duplication of proneural genes
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The Drosophila Achaete-Scute Complex (*AS-C*) comprises four genes, *achaete* (*ac*), *scute* (*sc*), *lethal of scute* (*l'sc*) and *asense* (*ase*) that encode transcriptional activators of the bHLH class. They are involved in neuronal specification and differentiation and are required for the development of the central and peripheral nervous system. In Dipteran flies the expression patterns of these genes is precisely controlled and determined by positional information given by upstream regulators. They activate specific genes (or combinations of genes) through the abundant cis-regulatory elements within the complex. As a result the location of sensory organs (e.g. the large bristled on the notum) is highly stereotyped. Three of the genes (*ac*, *sc* and *l'sc*) have originated by tandem duplication within the Diptera from a single *achaete-scute-homologue* (*ASH*) ancestor. The gene duplications correlate with subfunctionalization and adquisition of new regulatory elements giving rise to the stereotyped phenotype seen in Drosophila, however the details of this process remain unknown.

The recent availability of genome data from several Drosophila species and other insects allows us to look at the evolution of this complex, both at the level of gene number and organization. Our analysis shows that achaete-scute genes remain clustered in all analysed species. The presence and organization of cis-regulatory elements, which are interspersed and sometimes shared between the genes, explains the high conservation of the complex between all 12 sequenced Drosophila species. The analysis of other more divergent insects shows that the *AS-C* originated from a single *ASH* gene and a second *ase* gene already present in the ancestor of the insects. Surprisingly the duplication of *ASH* is not restricted to the Drosophila lineage but has occurred independently in other insects, and might be related to functional diversification in different lineages.

The inevitable ascent of Y chromosomes
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In species with XO males and XX females, the fusion of an autosome with an X chromosome, can give rise to a Y-chromosome. Such a neo-XY system can become established by the fixation of the fusion in part of the species range; either by genetic drift or by some forms of selection (perhaps due to the changed linkage). In either case the further spread of the neo-XY system throughout the species range is more difficult to explain, yet evolutionary analysis provides many examples where it appears to have occurred. This talk presents a new explanation for such an invasion, based on the proposal that the Y-chromosome has degenerated and is selected against in females. Once this has occurred, the neo-XY system will not spread if it is introduced into a new XO population at low frequency. Paradoxically, it will spread at a boundary where large populations of neo-XY abut on XO. In this case, the Y-chromosomes act as shock troops: they can move in large numbers into the XO population, where their fate is to be eliminated. Their sacrifice creates an environment in which the fused X is favoured and so the neo-XY system advances. Phylogeographic evidence for such an advance will be presented for the grasshopper *Podisma pedestris*.

Recombination, diversity, and divergence in the *Drosophila pseudoobscura* species subgroup
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One of the most influential observations in the past 20 years in molecular evolution has been the striking relationship of recombination rate and nucleotide diversity. Explanations for this relationship abound, but distinguishing among these explanations requires dissection of patterns of recombination and diversity at small scales. We report preliminary results from a set of such studies in the model system *Drosophila pseudoobscura*, wherein we have examined the relationship of recombination to both diversity and divergence from related species, looking both at a few focal regions and using genome-wide data. We found extensive fine-scale crossover rate heterogeneity, and fine-scale crossover rate correlates very strongly with both diversity and divergence. This relationship is strongest when small windows (<500kb or <200kb) are examined. Previous studies may have missed associations between crossover rate and diversity because crossover rate was estimated over windows that were too broad (so fine-scale rate variation was not captured).

Heterogeneous genomic divergence during speciation
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Genetic differentiation during speciation can be highly variable across the genome, with loci under divergent selection and those tightly physically-linked to them exhibiting stronger differentiation than neutral regions with little or no linkage to such loci. Moreover, adaptive divergence can increase genome-wide differentiation by reducing gene flow, thereby facilitating neutral genomic divergence via genetic drift. These signatures of divergent selection are now being reported in recently accumulating studies testing for 1) loci with higher levels of divergence than expected under neutrality, and 2) the association between levels of neutral differentiation between populations and the degree of adaptive phenotypic divergence ('Isolation-By-Adaptation'), respectively. A review and synthesis of these different sets of literature, coupled with our own empirical work on heterogeneous genomic differentiation between insect populations, will be used to illustrate how selection commonly affects differentiation via multiple mechanisms: directly, via linkage, and by facilitating genetic drift. The collective results thus illustrate the varied and sometimes non-intuitive contributions of selection to heterogeneous genomic differentiation. Finally, we present some alternative models for how regions of differentiation ('genomic islands of divergence') grow in size (i.e., how the effects of divergent selection spread from a few loci to the rest of the genome).

A clade-site method for detecting positive selection: dissecting the phylogenetics of adaptation.
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The clade-site method is a general approach for detecting shifts in the intensity of positive selection and in the codons responding. Analysis of several published examples of positive selection demonstrated that molecular patterns of adaptation are evolutionarily transient. Detection of these shifting patterns supports the view that positive selection acts on codons in a context-dependent manner that is likely driven by changes in the gene being studied and in the details of the selection.

The evolution of TEP1, an exceptionally polymorphic immunity gene in Anopheles gambiae
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Host-parasite coevolution can result in balancing selection, which maintains genetic variation in the susceptibility of hosts to parasites. In the mosquito *Anopheles gambiae*, it has been suggested that variation in a thioester-containing protein called TEP1 may alter its ability to transmit *Plasmodium falciparum* (the causal agent of Malaria). Strikingly, the high divergence between alleles of the TEP1 gene rivals that of the vertebrate MHC locus, where balancing selection has resulted in the long-term coexistence of ancient alleles. We studied whether TEP1 could be a case of ancient balanced polymorphism. However, our data suggests that the high divergence between alleles is probably not due to balancing selection, but may result from genetic exchange between TEP1 and other TEP loci. In fact, the TEP1 gene appears to be a chimera produced from at least two other TEP loci, and the divergence between TEP1 alleles most likely originates from two independent gene conversion events from one of these other genes. Nevertheless, TEP1 still shows evidence of natural selection, which has caused recent changes in the frequency of alleles. This indicates that there are functional differences between the alleles, and it remains possible that these differences may alter the susceptibility of mosquitoes to pathogens such as *Plasmodium*.

Overdominant selection at sex-linked loci and the long-term maintenance of males with hermaphrodite crustaceans

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Males should be at an evolutionary disadvantage when they occur with partially self-fertilising hermaphrodites. Accordingly, this sexual dimorphism is very rare. However, in branchiopod crustaceans, males have apparently persisted with hermaphrodites in multiple diverging lineages for at least 20 million years. To explain this ancient dimorphism, I will present a model that invokes overdominant selection at sex-linked loci. Published lab-based fitness assays for one species of branchiopod are consistent with the overdominance hypothesis, as are genotype frequencies in its natural populations.

The effect of new transposable element insertions on gene expression profiles

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Background: Many genomes contain a substantial number of transposable element (TE) insertions. A few of these TEs have been shown to be involved in gene regulation and the recent observation that many conserved non-genic elements have similarities to known TEs has led to the suggestion that TEs may be an important source of mutations which affect gene regulation. **Methodology/Principle findings:** Here we investigate this hypothesis by testing whether gene expression divergence between mouse and rat is correlated to the numbers of new transposable element insertions near genes in those species. We show that expression divergence is significantly correlated to the number of new LTR and SINE elements, but not to the numbers of LINEs. We quantify the effect and estimate that on average TE insertion has accounted for ~20% (12%,26%) of all expression profile divergence in rodents. **Conclusions:** These results suggest that TEs play a major role in gene expression evolution in rodents.

Evolution of species range in spatially and temporarily varying environments

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Two principal mechanisms have been proposed to explain limits to species range in a single-species scenario: maladaptive gene flow from central to marginal populations and constraints on genetic variance. We assess the ability of populations living in spatially structured environments to adapt in a quantitative trait as the environment changes in time; derive formulas for the predicted change in trait mean over time and space, compare the results to a single population and discuss the evolution of genetic variance.

Life-history traits drive the rates of accumulation of slightly-deleterious mutations in mammalian coding elements

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Life-history traits drive the rates of accumulation of slightly-deleterious mutations in mammalian coding elements After the effective size of a population, Ne, declines, some slightly deleterious amino acid replacements which were initially suppressed by purifying selection become effectively neutral and can reach fixation. Firstly we investigate this phenomenon for a set of all 13 mitochondrial protein-coding genes from 110 mammalian species. By using body mass as a proxy for Ne, we show that large mammals (i.e., those with low Ne) as compared with small ones (in our sample these are, on average, 369.5 kg and 275 g, respectively) have a 43% higher rate of accumulation of nonsynonymous nucleotide substitutions relative to synonymous substitutions, and an 8–40% higher rate of accumulation of radical amino acid substitutions relative to conservative substitutions, depending on the type of amino acid classification. These higher rates result in a 6% greater amino acid dissimilarity between modern species and their most recent reconstructed ancestors in large versus small mammals. Because nonsynonymous substitutions are likely to be more harmful than synonymous substitutions, and radical amino acid substitutions are likely to be more harmful than conservative ones, our results suggest that large mammals experience less efficient purifying selection than small mammals. Furthermore, because in the course of mammalian evolution body size tends to increase and, consequently, Ne tends to decline, evolution of mammals toward large body size may involve accumulation of slightly deleterious mutations in mitochondrial protein-coding genes, which may contribute to decline or extinction of large mammals. (Popadin, Polishchuk, Mamirova, Knorre & Gunbin 2007. Accumulation of slightly deleterious mutations in mitochondrial protein-coding genes of large versus small mammals. PNAS 104: 13390-13395). Secondly, using the ENCODE nuclear sequence data we estimated mammalian neutral evolutionary rates, approximated by the rate of fixation of synonymous (silent) substitutions per synonymous site (dS), and selective coefficients acting on Conserved Coding and Non-coding elements. We show that neutral evolutionary rates can be explained by the Generation Time (GT) hypothesis. Primates (especially humans), with their longer GT than other mammals, display a slowdown in the rate of fixation of silent substitutions. The evolution of constrained elements, particularly of non-synonymouse sites, fits well the expectations of the nearly neutral theory of molecular evolution. We show that rates of accumulation of non-synonymous substitutions per nonsynonymous site (dN) are dependant on a species-specific population size (Nikolaev, Montoya-Burgos, Konstantin Popadin, Parand, Margulies, NISC Comparative Sequencing Program & Antonarakis 2007. Life-History Traits Drive the Evolutionary Rates of Mammalian Coding and Non-Coding Genomic Elements. in press). Now, we are planning to reveal the next topics: (1) – What is the difference in generation time effect, for mitochondrial versus nuclear genes? (2) – What is the preferable localization of sites in which accumulation of slightly-deleterious mutations is more pronounced? (3) – Is there effect of accumulation of slightly-deleterious mutations associated with speciation (at the time of bottleneck)?

Phylogeography of caddisflies: identification of the processes underlying high diversity and endemism in the Balkans

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The impact of Pleistocene climatic changes on the biogeography of European freshwater fauna is still far less understood than in the case of terrestrial taxa. Similarly, the processes underlying biodiversity and speciation in refugial regions, especially the Balkans, seem to be more complex than originally recognized yet little studied. The Pleistocene is generally regarded as a time of very little diversification at the species level, although some recent studies have demonstrated a Pleistocene origin for some taxa. The Dinaric area is recognized as a European biodiversity hotspot and renowned for its high endemism. We performed phylogenetic and population genetic analyses on mitochondrial DNA sequences (COI and 16S) of several range-restricted Dinaric caddisfly endemics (*Drusus*, *Limnephilidae*, *Trichoptera*) in order to test the hypothesis that Pleistocene glaciations have promoted speciation and diversity in a refugial area. The divergence of five endemic Bosnian species and 11 populations of a Croatian taxon date to well within the Pleistocene period (1.25-0.43 Mya). Spatial analysis of molecular variance and nested clade analysis of the Croatian populations revealed very restricted gene flow on a small spatial scale and allopatric fragmentation. Given their limited dispersal ability, specific habitat requirements and life history traits, the present distribution of these species/populations in isolated sky islands likely represents the situation typical for interglacial phases. Dispersal is probably limited largely to glacial periods when the species descend in altitude to track suitable environmental conditions. Overall, the results suggest that the divergence of populations and formation of endemic species was promoted by allopatric fragmentation during interglacial periods, emphasising the importance of Pleistocene cyclic climatic change in generating diversity and endemism in refugial regions.

Range expansion depletes heritability of a major plant life-history trait

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Hexaploid populations of the annual herb *Mercurialis annua* expanded their geographic distribution, probably following glacial retreat, through migration from a refugium in North Africa up the east and west coasts of the Iberian Peninsula. Consistent with this interpretation, northern populations display much lower neutral genetic diversity than their southern counterparts, suggesting the impact of successive colonisation bottlenecks. Here we show, on the basis of artificial selection experiments in sixteen populations of *M. annua*, a clear decline in the heritable variation of the male reproductive effort towards the margins of the species' hexaploid range. Our results show that additive genetic variation for life history traits may be severely depleted during range expansion and that the ability of species to adapt to environmental change may be compromised at its range margins.

Conservation genetics of the endangered Mauritius parakeet

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The Mauritius parakeet (*Psittacula eques*) population provides a unique research opportunity. This island endemic has recently been downgraded from Critically Endangered following a rapid recovery from approximately 20 individuals to over 300 birds in just 20 years. The population has been closely monitored throughout the recovery, with all known nesting attempts recorded and the majority of the population identifiable with a unique colour ring combination. A suite of microsatellites have been developed and optimised for this species. To date, 371 individuals have been genotyped at 11 loci, allowing allele frequencies and observed heterozygosity of the population to be determined. Field records that describe the recent bottleneck are supported by the detection of a heterozygosity excess under the Infinite Allele Model ($P<0.01$), although this was not detected under the Stepwise Mutation Model ($P>0.05$). Despite the close monitoring of the population a number of cases of extra-pair paternity have been suspected, and several instances have now been genetically confirmed. During the initial phase of the bottleneck the population sex ratio was skewed in favour of males 3-4:1. In addition to a large number of floating males in the population, each breeding female was often accompanied by a dominant male and one or two subordinates. Genetic data can now shed new light on field records that describe the observed behaviour of these extra males. A sympatric population of ring-neck parakeets (*Psittacula krameri*) also occurs on the island and their population is now estimated to number approximately 35,000. Preliminary genotyping of the ring-neck parakeets has revealed not only that all markers developed for the *Mauritius parakeet* amplify in the ring-neck parakeet, but also that they share similar allele sizes. Given the overlapping distribution between populations, highly similar morphology and apparent genetic similarities, introgression between the endemic and introduced species cannot be ruled out.

The use of higher-order gene identity coefficients in population genetic studies

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Most studies involving relatedness or inbreeding use statistics based upon the sampling of two alleles, for example, the inbreeding coefficient F. Statistics based upon the sampling of triplets and quadruplets of alleles can be used for interesting and sometimes novel population genetic inferences. We discuss several applications of these coefficients in the study of mating systems, clonal population structure, landscape genetic structure, genetic distance, polyploid genome structure, and bottleneck effects. In one example, in yellow cedar, we found that clonal ramets (as compared to non-clonal individuals) contributed excessively to local inbreeding and relatedness.

Mating patterns in fragmented landscapes: a case study of a neotropical tree
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Habitat fragmentation is a pervasive evolutionary force directly reducing population sizes, increasing isolation and altering habitats. Island biogeographic theory predicts loss of genetic variation and increased divergence through drift (and selection) in small isolated fragments. The genetic impacts in terrestrial ecosystems remain unclear because the resultant landscape matrix varies in permeability. In addition, species life-history-traits influence the ability to persist and move through altered landscapes. Contradictory to predictions some species show increased gene flow through cleared landscapes, suggesting that drift may not reduce genetic variation. In an attempt to understand the complexity of these biological processes in neotropical trees the EU funded SEEDSOURCE project is actively researching the mating patterns of multiple species over a range of landscapes. The focus of this talk will be Pachira quinata (Bombacaceae), an economically important timber tree in Central America. It has the potential for long distance dispersal by bat-pollination and wind-dispersed seed in largely fragmented landscapes. Inbreeding is possible through bi-parental mating and a leaky self-incompatibility mechanism. As such we predict increased pollen dispersal, fewer sires and greater inbreeding in isolated trees and small isolated populations, compared to large continuous forests. We have compared mating patterns in two different systems: (1) fragmented landscape of varying population sizes and level of isolation, and (2) large continuous forest versus remnant trees in pasture. In support of predictions we found a trend for lower outcrossing rates in the pasture population due to high proportions of selfed seed on some trees. In contrast to predictions we found similar numbers of sires contributing to seed production in fragmented and continuous populations. Large pollen dispersal distances across the fragmented landscapes mean that genetic drift is unlikely to reduce variation in the long-term. We discuss the impact of different landscape matrices as barriers to pollen dispersal for contrasting species life-history-traits.

Genetic diversity of the planktonic foraminifera in the Arabian Sea
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Foraminifera are the most abundant of the marine protists. These unicellular eukaryotes are characterised by their calcareous shell, or test, the morphology of which varies enormously between species. With a fossil record spanning over 130 million years, they can be used to date sedimentary rocks and archive past climate. There have been many genetic studies of the planktonic foraminifera, providing valuable information on their genetic diversity across the global ocean. Until now however the Arabian Sea, at the uppermost point of the Indian Ocean has remained one of the last places to be sampled. In this study a transect was taken through this unique marine environment in order to examine the planktonic foraminifera present and to assess their genetic diversity. The results of this study revealed unprecedented levels of genetic diversity in the planktonic foraminifera of the Arabian Sea. Several novel genetic types have been discovered and some species have been sequenced for the first time.

Leaping (or sliding?) between peaks of co-adaptation
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Many (but not all) species of bacteria exhibit selected codon usage bias in genes expressed at high levels. The preferred (optimal) codons are those best recognised by the most abundant tRNA species. However, for many amino acids the identity of the optimal codon differs among bacteria, with the identity and abundance of tRNA genes varying in a coordinated manner. The intriguing question is how this state of coadapation (between tRNA genes and codon usage) can have diverged among species. Changes in either the complement of tRNA genes or the codon usage of highly expressed genes alone would be maladaptive, and there is no mechanism to change both together. To investigate this we have examined the divergence of selected codon usage bias and tRNA abundance among genome sequences of Enterobacteria. For the amino acid proline, species occupy one of two different co-adaptive peaks. A coordinated change in Pro tRNA gene complement and Pro codon usage appears to have occurred on multiple occasions within this bacterial family.

The genetic basis of inbreeding avoidance in house mice

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Major histocompatibility complex (MHC) proteins are involved in the recognition of self/non-self at the molecular level. It has been hypothesised that this function could be expanded to the level of the individual, signalling the relatedness of potential mates and thus facilitating the avoidance of inbreeding. Major Urinary Proteins (MUPs) are highly polymorphic molecules that account for 99% of the protein content of male mouse urine. A MUP profile could therefore act as an alternative signal for assessment of familial relationships. Our study was designed to investigate mating behaviour in semi-natural populations of full- and half-sibling wild-derived mice. We allowed the mice to mate freely in large outdoor enclosures and used a panel of microsatellite markers to construct a complete pedigree allowing us to observe biases in number of matings and offspring production per mating. We observed a significant reduction in the number of offspring produced from full-sib vs. half-sib matings. This supports the hypothesis that there is a deleterious effect of inbreeding. There was no evidence of MHC disassortative mating and no MHC homozygous deficiency in the offspring. This is in contrast to previ ous laboratory based experiments. By contrast, we show that females mate significantly less with males that have identical MUP genotypes.

Fire ants in Australia: Determining the origin of *Solenopsis invicta* Buren (Hymenoptera: Formicidae)

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Introduced populations of the red imported fire ant, *Solenopsis invicta* Buren (Hymenoptera: Formicidae), have proven to be a significant and costly pest in the United States. In 2001 fire ants were discovered in two regions in Brisbane, Australia, sparking a nationally funded eradication program. To assist in preventing further incursions it is necessary to understand the original invasion, primarily where the Australian *S. invicta* populations came from, and subsequently whether they arrived during a single or multiple introduction events. Phylogenetics, using mtDNA (COI), was used to examine *S. invicta* populations from native South American populations, and introduced populations in the United States and Australia. Australian populations showed very low diversity with only two divergent haplotypes found. Both of these haplotypes are identical to those found at multiple sites within the United States, suggesting the North American origin of Australian fire ants. *S. invicta* exists in either single queen colonies (monogynous) or as colonies with multiple queens (polygynous). RFLP analysis of *General protein-9* (*Gp-9*) was used to determine social form in Australian *S. invicta*. There were significant differences in social form between different geographic regions, supporting the hypothesis that there have been multiple introductions to Australia. This is further supported by microsatellite analysis, which shows a high level of assignment of individuals to different regions. By inferring the origin and frequency of *S. invicta* introductions into Australia we can focus quarantine procedures and aim to minimise further incursions of this costly invasive species.

A new likelihood based method to test tetraploid inheritance models: Rorippa hybrids show inheritance patterns intermediate between disomic and tetrasomic

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Traditionally, segregation in tetraploids is discussed in terms of its two extreme forms: disomic and tetrasomic inheritance. The former occurs in allotetraploids and results from strict preferential pairing between the homologous chromosomes in an exclusively bivalent meiotic configuration. The latter occurs in autotetraploids and can result from random pairing of chromosomes in either a bivalent or quadrivalent configuration. Mixed (or intermediate) inheritance models are to be expected if the homologous chromosomes have some, but not a strict pairing affinity. This could particularly apply to newly formed hybrids between species that are similar enough to allow successful hybridisation, but divergent enough to earn their species status. Although some authors had previously suggested the existence of intermediate inheritance, this has never been tested statistically, because a method to do so was unavailable. We present a simple likelihood-based approach that is able to incorporate disomic, tetrasomic and intermediate inheritance models. Our model shows that inheritance of microsatellite markers in natural tetraploids of R. amphibia and *R. sylvestris* is tetrasomic, corroborating previous suggestions of their autotetraploid origin. However, in F1 hybrids inheritance was intermediate to disomic and tetrasomic inheritance. In meiosis, chromosomes apparently paired preferentially with the homolog from the same parental species, but not strictly so. The occurrence of double reduction gametes indicated that quadrivalent formation occurs. Furthermore, we tested the general applicability of our model using published segregation data. In one case, an intermediate inheritance model gave a better fit to the data than the tetrasomic model advocated by the authors. The existence of inheritance intermediate to disomic and tetrasomic has important implications for linkage mapping and population genetics and hence breeding programs of tetraploids. Methods that have been developed for either disomic or tetrasomic tetraploids may not be generally applicable, particularly in systems where hybridisation is common.

The applied population genetics of *Populus*: transgenes, exotic species, gene flow, markers, and more

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Before any broad release of poplar as a new source of biofuel and bioproducts can be considered, the potential environmental impacts must be firmly established. We are tackling this issue through an integrative approach that includes risk assessment through population genetic modelling, teamed with studies of gene flow in both plantations and natural populations of native poplars. Our major accomplishments to date include the development of a model that reinforces the importance of natural population genetic structure to the risk of transgene escape and fixation. Through the high-throughput genotyping of ~4800 progeny collected over three years, we have demonstrated that genes from exotic poplar species (e.g. *Populus nigra*, *P. maximowiczii*, *P. trichocarpa*) are passed to native poplars (*P. balsamifera* and *P. deltoides*) near plantations. This rate of hybrid formation varied with site, species and year, ranging from 3-62 %. Additional genotyping of 42 SNPs from 636 native poplars from natural contact zones throughout Quebec showed that hybrids form in disturbed, ruderal environments at a rate of 2.9%, and that second generation hybrids are consistently biased toward *P. balsamifera*. In parallel, DNA sequencing of 38 trees in a complex prairie ecosystem has shown that the poplar hybrids planted as windbreaks by early pioneers, which included germplasm from two exotic species (*P. laurifolia*, *P. nigra*) have escaped and gone feral. Recent work has expanded our marker set, through the data-mining of microarray experiments conducted on host-pathogen interactions in hybrid poplars (including transgenic lines) and literature surveys. We have screened a subset of these candidate genes by sequencing collections of *P. balsamifera* and *P. deltoides* individuals that transect their native ranges. This coming year, we will genotype 1500 individuals of *P. balsamifera* for 100 SNPs to study the genetic structure of natural populations and evaluate molecular evidence for adaptation. A preliminary comparison of patterns of nucleotide substitution among North American poplar species suggests the action of purifying selection at several of these genes. The potential environmental impact of transgenic poplar needs to be considered in the context of the extensive introgression that already exists within natural populations and the degree of selection on the transgenes themselves.

Host-driven speciation in a parasitic plant

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Orobanche (broomrapes) are obligate parasites which attach to the roots of other plants as seedlings. Each species has a preferred host-range and while some species parasitize a variety of plants, others are highly host-specific. It is possible that speciation in parasitic plants, like Orobanche, might be triggered by a shift in host preference. Using a four-pronged approach, we are investigating whether host-driven genetic divergence may be isolating populations of *O. minor* in the UK and northern France. Molecular marker (ISSR) data and morphometric data indicate that populations specifically parasitizing wild carrot (*Daucus carota*), or clover (*Trifolium pratense*) may be ecologically isolated. Sequence characterized amplified region (SCAR) markers are currently being used to construct a phylogeny of these host-specific races to investigate whether cryptic species may be defined by their host range. Finally, host specificity of *O. minor* is being assayed by cultivating host and parasite together in vitro using 'rhizotron' petri dish bioassays and histological techniques. Our data suggest that host-driven isolation may be an important mechanism for speciation in parasitic plants such as Orobanche.

LAPDOG - a tool for generating orthologous nucleotide datasets and application of these datasets in genomic studies.

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LAPDOG is a tool that produces nucleotide-based orthologous gene alignments from complete genomes, and provides a user-friendly interface for the utilisation of this dataset in primer design. The possibilities with this tool are multiple. The dataset can form the basis of comparative genomic analyses, diversity analyses and phylogenetic analyses. Primer design allows wide-ranging, cross-species studies of non-model organisms. A key element of primer design is that nucleotide sequences are used. This led to the development of a nucleotide-based orthology detection method, which further analysis suggests may be more informative than the traditional protein-based methods for closely related organisms.

A natural transgenic plant

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In some Swedish populations of *Festuca ovina*, the nuclear gene *PgiC* was found in two copies in about 10% of the plants. The second copy, *PgiC2*, was later found to not be the result of gene duplication but have been horizontally transferred from another grass species, *Poa palustris*. This horizontal gene transfer has now been studied both in a geographic and molecular context. We collected *F. ovina* populations in Denmark, Germany, Poland and eastern Sweden. These were analysed for presence of the transgene *PgiC2* and we discovered that the natural transgenic *F. ovina* plants are not unique for southern Sweden. We have found transgenic plants in Germany, eastern Denmark (Bornholm), Poland and eastern Sweden (Öland). One population in Öland has a frequencey of natural transgenes as high as 67%. We have also performed genome walking in order to find out how much genetic material was transferred. The first 1000 bps upstream of *PgiC* in *P. palustris* and *PgiC2* in *F. ovina* are more or less identical. After this point the sequences no longer align at all. The 300 bps upstream of this point can be used as a marker for *PgiC2*. We tested several other *Poa* and *Festuca* species for this marker, but none of the other *Festuca* species or any of the diploid *Poa* species has it. Surprisingly all of our polyploid *Poa* species held this sequence, however, not at the same location as in *F. ovina PgiC2*. We have not yet discovered the identity or function of these 300 bps, but ongoing studies will hopefully reveal if the same feature can be found downstream of the gene. If so, we might be able to say something about the mechanism behind the transfer; if indeed we have found a horizontally transferred gene flanked by transposable elements of some kind.

Mapping melanism in the peppered moth

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The rise and fall of the melanic morph of adult peppered moths (*Biston betularia*) is among the best documented cases of the spread of a mutation in natural populations, but the actual molecular genetics and developmental mechanism underlying this classic polymorphism remains to be described. Beyond understanding the developmental pathway, this study is aimed at resolving outstanding questions about the evolutionary origins of this widespread polymorphism, and of detecting a selective sweep associated with industrial melanism. We will present a first generation linkage map for *Biston betularia* (carbonaria), based primarily on AFLPs and including the major gene candidates for insect melanisation

Evidence of selection on rDNA in the *Podisma pedestris* hybrid zone

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The two chromosomal races of the grasshopper *Podisma pedestris* (the XO and Neo-XY), where first described in 1970 and the hybrid zone between them was discovered soon afterwards. Extensive ecological and analytical investigations led to the conclusion that the hybrid zone is maintained by selection on many genes of small effect. Yet no other consistent differences were found between the races in surveys of various morphological, allozyme and cytogenetic markers. However, I have recently shown that there is an extraordinary degree of variation in the chromosomal location of the rDNA loci, both within and between populations. I have previously reported that this variation can be used to divide populations into distinct cytogenetic races, some of which take part in hybrid zone formation. In this presentation I describe an analysis of the different rDNA loci in the hybrid zone, which reveals that they are not mixing neutrally, but instead, show assymetrical introgression. Biological reasons behind this type of mixing are discussed and their relevance to other hybrid zones is assessed.

The genetic basis of inbreeding depression: Case studies of adult lethality in Drosophila

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Severe inbreeding can lead to the genetic fixation of heritable diseases which preclude a healthy life course. Many of these genetic defects are expressed as severe increases in age-specific mortality, accelerating ageing and ultimately curtailing lifespan. We aim at unravelling, at a detailed and mechanistic level, the genetic basis of inbreeding depression in lifespan using a fruitfly model (*Drosophila melanogaster*). We have analysed two instances of inbreeding-related lethality by performing a quantitative trait loci (QTL) mapping experiment and detected the QTL underlying our lethal inbreeding effects. We found a single locus to condition the lethal effect in the temperature sensitive inbred line (LI4) and two loci to underlie the lethal effect in the cold sensitive line (LI10). The respective QTL may consist of one gene, or alternatively include several closely linked genes. All lethal alleles were recessive or nearly so, which fits the idea that inbreeding depression is caused by the expression of recessive deleterious alleles. The simple genetic basis of these effects is encouraging with respect to future research.

Matrilineal clusters reflect female philopatry in snow voles
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Sex specific dispersal strategies are thought to have evolved under a variety of different selective pressures acting differently on both sexes. In this study we aim to bridge the gap between theory and observational data on the evolution of dispersal and philopatry by combining ecological and genetic data within a natural population of snow voles (*Chionomys nivalis*) in the Swiss Alps. Unlike other microtine species, snow vole exibit stable population dynamics with little annual variation in density and a low reproductive output. Extensive capture mark re-capture data and molecular paternity analyses revealed a female biased adult sex ratio, promiscuous mating system, strong female philopatry and male biased dispersal. This suggest different evolutionary costs of leaving and staying in the natal area for males and females.

In high demand: Synonymous sites face conflicting selection pressures at exon-intron boundaries
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In *Drosophila melanogaster*, synonymous codons corresponding to the most abundant cognate tRNAs are used more frequently, especially in highly expressed genes. Increased use of such “optimal” codons is considered an adaptation for translational efficiency. At the same time, one finds that some synonymous codons are relatively more abundant in the vicinity of exon-intron junctions. In principle, this finding can be explained both by Hill-Robertson effects and selection for information necessary to enable correct splicing. However, several results support the splicing model over Hill-Robertson interference: A) trends in codon usage are strikingly similar to those in mammals in which codon usage near boundaries correlates with abundance in exonic splicing enhancers (ESEs), B) codons preferred near boundaries tend to be A-rich and C-poor, as expected were ESEs involved, C) codons preferred near boundaries are typically not translationally optimal. Thus, translationally optimal codon usage is compromised in the vicinity of splice junctions in intron-containing genes. On the gene level, however, controlling for known correlates of codon bias, the impact on codon usage patterns is quantitatively small.

Long-distance dispersal and adaptation to host resistance in a heterogeneous environment
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One strategy in plant breeding is to introduce single resistance alleles into lines with agronomic valuable traits. This type of resistance is generally quickly overcome by pathogens that mutated to virulence. When such a virulent genotype emerges, its frequency normally increases rapidly as it has a selective advantage by having a broader host range than its avirulent competitors. This is especially true for pathogenic fungi with small spores, e.g. the rust and the mildew pathogens, that can be dispersed by wind over long distances, infecting host plants at new locations hundreds of kilometres away. Frequencies of single virulent pathogen clones reported in field studies can be extremely high, even when the frequency of the formerly resistant host is much lower (Brown and Hovmoller, 2002). To understand the underlying population processes we extend an individual based computer simulation of pathogen dispersal (Wingen et al., 2007) to a heterogeneous environment. We model the interaction of selection and dispersal by a simple setting consisting of two patches: a non-selective source patch (e.g. a susceptible crop) and a selective target patch (e.g. a hitherto resistant crop). Pathogens can gain virulence by a mutation in only one of their 32-biallelic loci and are dispersed according to either a power-law function, particularly relevant to long-distance wind dispersal, or an exponential function of similar median dispersal distance. The resulting population structure is mainly affected by three parameters: 1) the immigration rate; 2) the mutation rate; 3) the time to fill the newly colonised space. Moreover, the immigration rate is dependent on the distance between patches and the type of dispersal function, with power-law functions generating more rare migrants than exponential functions, resulting in distant patches becoming filled with single genotypes. The results from simulations using different dispersal types, patch distances and mutation rates help to explain the observed patterns of population structure in wind-dispersed pathogens in fieldstudies. More complex simulations with multi-patches are in progress to investigate the generality as well as the limits of predictions from the simple two-patch scenario. Brown, J. K. M. and Hovmoller, M. S. (2002). Aerial dispersal of pathogens on the global and continental scales and its impact on plant disease. Science, 297:537-541. Wingen, L. U., Brown, J. K. M., and Shaw, M. W. (2007). The population genetic structure of clonal organisms generated by exponentially-bounded and fat-tailed dispersal. Genetics , 177:435-448

Connectivity in an ephemeral Australian river system: Population genetics meets otolith chemistry.
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Unpredictable flows and small gradient anabranch channels are defining features of Australian lowland rivers. Under low flow conditions these ephemeral channels are fragmented into disconnected waterbodies that provide refuge to instream fauna until connectivity is restored with annual rains. More recently barriers resulting from flow regulation (e.g. dams and weirs) have been shown to alter natural flow regimes and instream levels of connectivity. Using mtDNA (ATPase) and 9 nuclear loci we examined spatial and temporal levels of connectivity in the ubiquitous freshwater fish, *Retropinna semoni* across three lowland catchments of the Murray Darling Basin (MDB) in south-eastern Australia. Based on traditional frequency approaches, dispersal among even neighbouring populations within a catchment appears significantly restricted however no significant structure was detected among catchments. Both historical estimates of migration under a coalescent model and current movement patterns based on assignment testing suggest that limited dispersal , among even geographically close populations (<20km), results from intrinsic biological traits and/or natural instream fragmentation more so than current barriers associated with the infrastructure for water regulation. Restricted dispersal at this fine scale is further supported from results of otolith chemistry analysis that shows limited within lifetime movement for individuals in all three catchments.

Ecological and geographical drivers of speciation in the *Anopheles sundaicus* (*Diptera*: *Culicidae*) species complex
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The relative impact of ecology and geography in generating biodiversity, within and between species, remains controversial. For the *Anopheles sundaicus* mosquito species complex two competing hypotheses exist on how many species there are, and how speciation has taken place. Polytene chromosomal forms, and associated allozyme data, indicate that different chromosomal forms represent several sympatric species that differ in habitat salinity preference. In contrast, mitochondrial molecular data has been used to describe three allopatric species. We critically assessed the allopatric speciation theory by conducting a phylogeographic study of populations from mainland SE Asia, Borneo and Indonesia, using one mitochondrial and two nuclear markers. We infer that the populations have a recent common origin in North Sumatra, from where they migrated to the mainland and Borneo when the landmasses were connected during Pleistocene glacial periods. The lack of long-term isolation does not support the hypothesis that the geographically isolated populations have indeed speciated. The earlier allozyme studies indicated high differentiation between chromosomal forms at the mannose-6-phosphatase isomerase (Mpi) gene. We tested the association with ecological niche by sequencing Mpi (762/1298 bp) from sympatric brackish and freshwater populations, and found no association between genotype and larval habitat. This lack of congruence with the allozyme data casts doubt on the hypothesis of ecological speciation involving divergence at or around the Mpi gene. Alternative hypotheses to reconcile sequence and allozyme data are: that the Mpi gene is under long-term balancing selection, but the signal is obscured by recombination; or that Mpi has undergone environmentally-dependent post-translational modification.

Contrasting ancestral and extant polymorphisms in *Sonneratia*
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The level of DNA polymorphism in the ancestral species at the time of speciation can be estimated using DNA sequences from many loci sampled from two or more extant species. The comparison between ancestral and extant polymorphism can be informative about the population genetics of speciation. In this study, we collected and analyzed DNA sequences of ~60 genes from four species of Sonneratia, a common genus of mangroves on the Indo-Pacific coasts. We found that the 3 ancestral species were comparable to each other in terms of level of polymorphism. However, the ancestral species at the time of speciation were substantially more polymorphic than the extant geographical populations. This ancestral polymorphism is in fact larger than, or at least equal to, the level of polymorphism of the entire species across extant geographical populations. We suggest that, at the time of speciation, the ancestral species consisted of interconnected but strongly divided geographical populations. This population structure would give rise to high level of polymorphism across species range. This approach of studying the speciation history by genomic means should be applicable to non-model organisms.

Posters

Habitat mosaic effects spatial genetic structure and counters distance and gene flow potential in a generalist mammal species

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Many species exploit habitat patches of different kinds and quality within there home range. We address whether differences in local habitats influences their spatial genetic structure using the European wood mouse, Apodemus sylvaticus, in which both sexes frequently disperse distances over 1km. Natural populations sampled in inner forest, edge of forest and adjacent hedgerow locations, at three matched sites in winter (January to March), for variation at seven microsatellite loci, indicated that the population was highly structured across the three habitat types. There was no relationship between genetic and geographical distances at two of the three sites and a weak association at the third. Sampling in successive years confirmed genetic temporal stability. Genetic heterogeneity tests suggest that the association between genetic variation and habitat block arose independently at each site. Despite the absence of physical barriers to dispersal, habitat is a strong influence on population genetic differentiation. Under favourable conditions, this could lead to genetic isolation, a process accelerated by genetic drift where effective population size is reduced. This finding has major implications for understanding the population dynamics and dispersal of habitat generalists, and is critical in understanding the dynamics of populations occupying discrete, variable habitat patches.

Implications of the first brown algal genome sequence (*Ectocarpus siliculosus*) for marine population genetics.

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The brown algae, or seaweeds, are responsible for the bulk of primary production in coastal and intertidal areas, but no representative genome sequence is currently available and our ability to address fundamental questions is, accordingly, limited. This is now changing and I will discuss the uses to which we hope to put the first brown algal genome sequence, that of *Ectocarpus siliculosus*.

Inference of matrilineal pedigrees under partial selfing (IMPPS).

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A simple population genetic model is presented for a hermaphrodite annual species where male gametes (pollen) typically disperse much further than seeds. The selfing rate is a parameter of the model. Under this model, the pedigree of a sample from a single locality is loop-free. A novel Markov chain Monte Carlo strategy is presented for sampling from the joint posterior distribution of the pedigree of such a sample and the parameters of the population genetic model (including the selfing rate) given the genotypes, at unlinked marker loci, of the sampled individuals.

Sheffield Molecular Genetics Facility
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The Sheffield Molecular Genetics Facility (SMGF) 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 is supported by NERC however application for access to facilities and training is welcome from NERC and non-NERC grant holders. The main call on the Facility at Sheffield remains to be for the development and application of sets of genetic markers for use in population genetics and behavioural ecology, and in particular the use of enrichment methods to develop microsatellite marker sets. The Facility includes an Applied Biosystems model 3730 48-capillary DNA analyzer, which is used both for sequencing and the automated genotyping of microsatellites. The Facility also supports other applications, including multilocus and single-locus minisatellite DNA fingerprinting, DNA sequencing, AFLP analysis and sex-typing (eg birds), and is prepared to consider extending the range of available techniques, by discussion. Projects that contribute to the training of research students or others are encouraged to apply. Successful applicants are provided with training and access to the SMGF molecular genetics facilities free of charge for an approved time period. No charge will normally be made for using consumables or equipment in the Facility, but users must make separate arrangements for their accommodation and travel costs. If you would like any more details or wish to make informal enquiries regarding the feasibility of your application please email Deborah Dawson, D.A.Dawson@Sheffield.ac.uk. Contact Information: Sheffield Molecular Genetics Facility, Department of Animal and Plant Sciences, University of Sheffield, Western Bank, Sheffield, S10 2TN, UK Homepage: http://www.shef.ac.uk/misc/groups/molecol/smgf.html Head of Facility: Professor Terry Burke, Email: T.A.Burke@Sheffield.ac.uk, Tel: 0114 222 0096 Facility Co-ordinator: Deborah Dawson, Email: D.A.Dawson@Sheffield.ac.uk, Tel: 0114 222 0106

Population genetics of adaptation of the Asr gene family in wild tomatoes.
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Wild tomatoes species are a valuable evolutionary model for the study of drought tolerance because they grow in a large range of environments, from mesic to arid. For a better understanding of the genetic basis of drought tolerance adaptation in wild tomatoes, we sequenced the candidate genes *Asr1* and *Asr2* in populations from the two closely related species *S. chilense* and *S. peruvianum*. Members of the Asr gene family are involved in drought tolerance pathways and are up-regulated in water-stressed plants. They are supposed to act as transcription factors in the ABA (abscisic acid) pathway. Since the studied populations were collected in contrasted habitats regarding to water availability, we expected to detect a population-dependant pattern of selection on *Asr1* and *Asr2*. Several tests of neutrality (Tajima's *D*, Fu and Li's *D*, Fu and Li's *F*) show hints for positive selection on the Asr2 gene in S. peruvianum, especially in the population from the more mesic environment (Canta). Additional analyses were performed to account for the demographic history of the sample. In particular, the isolation model by Wakeley and Hey was applied on neutral locus data to infer the speciation parameters of our *S. chilense* and *S. peruvianum* sample. We compared these parameters values to those obtained from *Asr1* and *Asr2* and were able to better precise the evolutionary history of *Asr1* and *Asr2*.

Differentiation among populations of an intertidal snail: the importance of size and habitat
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We used AFLPs to determine the genetic structure of three different parapatric morphs of Littorina saxatilis and the degree of introgression between them. We scanned for signatures of natural divergent selection within the AFLP data set. Finally, we review the taxonomic status of *Littorina neglecta*.

Multiple linked tail to head oriented ß and a globin genes in atlantic cod, *Gadus morhua*
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Allozyme variation in Atlantic cod hemoglobins shows various signs of natural selection. Sick (1965) described a system consisting of two major zones of hemoglobin in Atlantic cod, HbI and HbII. The HbI zone shows variation interpreted genetically as a polymorphism with a pair of co-dominant alleles F and S, a case of a simple single-locus two-allele balanced polymorphism. In order to understand and explain structure and function of hemoglobin proteins and selection at their genes in Atlantic cod we report here a ?rst step of characterizing the molecular components. The a and ß globin genes are oriented tail to head in a 5 to 3 direction with 1500 base pairs intergenic region. Using a PCR/population-genetics strategy for genomic exploration we attempt to estimate the number of linked ß and a globin genes. To deal with PCR errors we used doubleton and triplet phylogenetically informative sites and found ten clusters of linked ß/a globin genes in the genome of Atlantic cod. These different gene sets in the genome may represent different loci encoding different globins and/or allelic variation at some loci.

Landscape Genetics of a recovering European otter (*Lutra lutra*) population
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Bayesian clustering analysis of a recovering otter population in Wales has identified two populations of otters but with no obvious barrier to gene flow evident between them. Spatial and landscape genetic techniques are being applied to correlate microsatellite data from RTA-sampled otters from across Wales and the bordering regions of England with fine-scale landscape features. Resistance-to-movement surfaces have been developed based on landscape data to produce least-cost paths among individual georeferenced genotypes. Dispersal cost matrices are computed based on these least-cost paths, allowing the identification of a combination of environmental factors that appear to drive and restrict gene flow in a rapidly recovering species and an anthropogenically altered landscape.

Mating system evolution in *Arabidopsis lyrata* ssp. *Lyrata*
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In reproductive strategies in most organisms, outcrossing is favored over inbreeding in terms of fitness costs. The masking of recessive deleterious mutations by dominant non-deleterious ones, and heterozygote advantage, in which heterozygous individuals are supposed to be fitter than homozygotes, are two theories that explain this difference in fitness. This raises the question of how selfing individuals maintain themselves within populations consisting of outcrossing and inbreeding individuals. *Arabidopsis lyrata* is a small plant that occurs on the Northern hemisphere. It is mainly outcrossing due to a genetically determined self-incompatibility system. Around the Great Lakes of North America, populations of *Arabidopsis lyrata* exist which differ in the ratio of individuals capable of setting selfed seed and which differ in their realised outcrossing rates. The loss of self incompatibility could be due to a difference in population history between selfing and outcrossing populations. Separate refugia during glacial periods could have resulted in independent post-glacial expansion. This probably had severe implications for genetic variation and mating availability within these populations.We are using this system to test whether there are fitness differences between (forced) selfed and outcrossed offspring from parents from predominantly selfing compared to predominantly outcrossing populations and if populations of *A. lyrata* around the Great Lakes have experienced different (recent) histories. We are conducting an experiment to evaluate inbreeding depression in relation to outcrossing history, using relative differences in reproductive parameters, life history traits and pathogen resistance of selfed and outcrossed progeny. We are using chloroplast DNA markers to evaluate scenarios of postglacial expansion, which could tell us more about the causes of loss of SI. Preliminary results show no differences in germination rates or seedling weights between selfed and outcrossed progeny from self-compatible parents but forced selfing results indicate that purging might have played an important role in maintaining a mixed mating system based on the difficulty of producing fruits with viable seeds from strongly self-incompatible individuals. Chloroplast DNA markers show a pattern of haplotypes which is independent of the populations' mating system, although most of the predominantly selfing populations share one of the three haplotypes found in the region. This suggests postglacial colonization of the area from different refugia but independent of the loss of SI.

Heracleum in Europe and Asia: genetic relationships between species in invaded and native distribution ranges

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Tall species of *Heracleum* were introduced into Europe from south-west Asia in the nineteenth century and are now widespread in many countries. To elucidate genetic relationships between these species and their populations we analysed samples collected from individuals of 72 populations in 15 European and four Asian countries. Using nine primer pair combinations we analysed 631 amplified fragment length polymorphism (AFLP) markers of 189 individuals representing the three invasive species from invaded and native ranges, two species native to Europe (*H. sphondylium*, *H. sibiricum*) and three species native to the Caucasus (*H. antasiaticum*, *H. leskovii* and *H. ponticum*). Neighbour-joining and principal coordinate analyses revealed that plants of each of the three taxa collected in the invaded range are genetically close with those from their native ranges. It also showed close genetic relationship of the three invasive Heracleum species in Europe, particularly between *H. mantegazzianum* and *H. sosnowskyi*. We detected high overall genetic variability in the invaded range. This suggests that these invasive species were not affected by genetic bottleneck on the continental scale and that rapid evolution, drift and hybridization may have played a role in genetic structuring of invading populations since the introduction of these species into Europe. On the other hand, individual populations in the invaded range had lower within-population variation than populations in the native areas. Thus, populations in Europe may be influenced by founder events and may be experiencing restricted gene-flow and higher inbreeding compared to native populations. Our results suggest that multiple introductions of all three species into Europe are most likely.

Testing for a signal of selection at olfactory receptor gene-linked markers in coho salmon (*Oncorhynchus kisutch*)

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Interest in the new field of population genomics has generated a growing number of studies which demonstrate the “power and promise” of examining populations through neutral genetic markers, as well as at loci under selection. In a previous study, using putatively neutral microsatellite markers, we described relatively weak genetic structure among wild coho salmon (*Oncorhynchus kisutch*) populations of the Oregon coast, U.S.A. We suspect that while demographic processes, such as migration, have attenuated structure at neutral loci, significant structure may exist at loci under selection. In this study, we characterize the genetic sequence of seven olfactory receptor genes from coho salmon, including both 5’ and 3’ flanking sequence. We then genotyped individuals from four hatchery populations at polymorphic markers linked to these genes, and tested for a signal of selection at these markers against a panel of putatively neutral microsatellites. In all pairwise tests, two or more olfactory receptor gene-linked markers appeared as “outliers”, suggesting that selection is occurring over these loci. Future work will examine diversity at these loci in wild populations, which have likely not been exposed to the same selection pressures as hatchery coho salmon."

The ribosomal DNA and R1/R2 retrotransposons insertions in the 28S rRNA genes are useful markers in population researches of german cockroach *Blattella germanica*.

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The nucleotide sequence and length of various structural elements of nuclear rDNA units are differentially conserved over evolutionary time, with the most stable being the rRNA genes and the most variable being the IGS. In many eukaryotic species the high variability of the IGS is due to short subrepeats that differ in both their nucleotide composition and position within IGS. Tandem localization of the evolutionarily stable 28S gene and variable IGS makes rDNA a potential candidate for investigations of intraspecific variation of IGS RFLP by blot-hybridization techniques. rDNA repeats may be located within one or a few chromosomes and are associated with the formation of the nucleolar organizer (NO). The NO of the German cockroach is located within the X-chromosome. Each cockroach male has only one X-chromosome (XO), while females have two chromosomes (XX). Therefore, polymorphic rDNA markers seen in *B. germanica* males correspond to a single X-chromosome, and each population can thus be characterized by both rDNA band (fragment) frequencies and haplotype (a particular X-chromosome pattern) frequencies. In this study, HindIII rDNA polymorphism was compared in individual insects from three cockroach populations collected in different pig farms. We describe the inheritance of the chromosome HindIII rDNA patterns during twelve generations (three years) of rearing in the laboratory and show stability of this polymorphic marker. Our results show that cockroach populations from relatively close geographic localities are genetically differentiated at the rDNA IGS repeats, consistent with human-aided dispersal, and again highlight the utility of the IGS for inferring regional relationships among populations within a species. Furthermore, the ribosomal gene clusters of practically all arthropods and, particularly, insects, contain R1 and R2 mobile elements. These elements belong to either non-LTR (non-long terminal repeat) retrotransposons, which do not contain LTRs, or to long interspersed nuclear elements (LINEs). The specific target sites of R1 and R2 are within the 28S rRNA gene. We identified intraspecies polymorphism in patterns of 5'-truncated copies of *Blattella germanica* R1 and R2 elements by using PCR with primers flanking the target sites for R1 and R2 retrotransposons. We observe inheritance of 5'-truncated copies in *B. germanica* males and females of the first generation obtained upon individual mating. Probably, the 5'-truncated copies showed stable Mendelian inheritance here. This assumption is likely to be true at a low frequency of both retrotransposition and recombination of transposable elements within the rDNA cluster. Moreover it was demonstrated intraspecies polymorphism of individual adult male cockroach from distinct populations. We suppose, that each population possess its individual 5' truncated copies patterns (haplotypes) which could be used in population researches. Thus, sequence variation in the ribosomal DNA is a useful marker, and RFLP of rDNA is a simple, robust, and reproducible technique for differentiating recently diverged cockroach populations."

Sexual system and genetic diversity in *Mercurialis annua*: a patch-level test of the metapopulation model

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Natural selection during and after long-distance colonisation events is predicted to favour the evolution of self-fertile hermaphroditism over dioecy, all else being equal. This idea has found empirical support in species that have undergone range expansion, have colonised oceanic islands, or persist in a regional metapopulation. In this project, we explore the scale of colonization from regional, population to patch level. We address the question: can variation in the sexual system at a patch level also be explained by a history of patch-scale colonisation? We have chosen to use Mercurialis annua as a study species because of the remarkable variation in sexual systems it displays, from monoecy through androdioecy (where males coexist with hermaphroditic plants) to dioecy. Androdioecious populations differ widely in their male frequencies at large and small spatial scales. Previous work has shown evidence for the importance of colonisation in shaping the sexual system and genetic diversity of populations at a large spatial scale. The aim of this project is to test the hypothesis that very fine-scale patterns of sex-ratio variation and genetic diversity in M. annua are also due to colonisation at a patch level. The populations we wish to study are allohexaploid making it impossible to utilize conventional analysis techniques for co-dominant markers. We have been successful in developing microsatellite markers that amplify in only one of the two genomes of this lineage. Currently, we are screening genetic variation in natural populations using these co-dominant diploid markers. We predict that, just as at the regional scale, patches with high frequencies of males will also show the highest levels of genetic diversity and lower levels of divergence.

Genetical control of expression divergence of duplicate genes

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Expression divergence of duplicate genes is widely believed to be important for their retention and evolution of new function, although the mechanism that determines their expression divergence remains unclear. We use a genetical genomics approach to explore divergence in genetical control of yeast duplicate genes created by a whole genome duplication that occurred about 100 million years ago and those with a younger duplication age. The analysis reveals that duplicate genes have a significantly higher probability of sharing common genetic control than pairs of singleton genes. The expression quantitative trait loci (eQTLs) have diverged completely for a high proportion of duplicate pairs, while a substantially larger proportion of duplicates share common regulatory motifs after 100 million years of divergent evolution. The similarity in both genetical control and cis motif structure for a duplicate pair is a reflection of its evolutionary age. This study reveals that up to 20% of variation in expression between ancient duplicate gene pairs in the yeast genome can be explained by both cis motif divergence (~8%) and by trans eQTL divergence (~10%). Initially, divergence in all three aspects of cis motif structure, trans genetical control, and expression evolve co-ordinately with the coding sequence divergence of both young and old duplicate pairs. These findings highlight the importance of divergence in both cis motif structure and trans genetical control in the diverse set of mechanisms underlying the expression divergence of yeast duplicate genes.

An evolutionary framework for systems biology

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Evolutionary population genetics has a long tradition of mathematical modelling in biology that frequently abstracts details. Molecular biology has a strong tradition of inferring molecular interactions from clear cut clever experiments that frequently do not require quantitative analyses. Both traditions have been incredibly successful in furthering our understanding of the natural world. However, after many decades of research some familiar assumptions are reaching their limits and evolutionary biologists get increasingly interested in the molecular details of their systems, while molecular biologists increasingly realize that quantitative modelling is actually worth the pain of understanding some equations. Many researchers in both fields feel that these are exciting times that almost redefine their field. While evolutionary biology has no agreed name for 'the new' (many have been suggested), molecular biology and cell biology have decided to use 'systems biology' to promote the new direction to their discipline. Here I am proposing that this new excitement for quantitative rigor in the description of intracellular processes could benefit from and contribute to attempts in evolutionary biology to understand more precisely the forces that have shaped the existing diversity of life.

Comparison of coding and non-coding sequences between *Drosophila miranda* and *D. pseudoobscura*

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Non-coding DNA comprises most of the *Drosophila* genome and has classically been thought to lack function and thus to evolve neutrally. However, recent studies have shown constraint in intronic and intergenic regions in *Drosophila*, in particular in *D. melanogaster* and *D. simulans*. *Drosophila miranda* and *D. pseudoobscura* are closely related, with a divergence time of about 2 My. Using BAC sequences available from *D. miranda* and including 179 genes, we calculated pairwise rates of divergence from *D. pseudoobscura* for different classes of sites, especially synonymous and intronic sites. We also investigated correlations of divergence with GC content and sequence length since such correlations have been found using *D. melanogaster* and *D. simulans*.

Olfactory receptor gene expression in *Drosophila*: species and tissue specific patterns of expression

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Chemoreception describes the process of sensing chemical signals and thus forms a major part of the interaction between an organism and its environment. In *Drosophila*, olfactory signals play a major role in habitat and mate choice, processes which generate prezygotic reproductive isolation, hence olfactory receptor (OR) genes are likely to play key roles in the speciation process. Although genome sequencing has identified coding sequence differences between several Drosophila species, any differences in gene expression of these loci among species remain unknown. This study investigates the relative gene expression differences of ORs on the 3R chromosome in three *Drosophila* species and utilises real-time PCR to generate both presence/absence and relative expression data. Results reveal species specific patterns of gene expression and evidence of tissue specific alternative splicing. ORs are also found to be expressed in the bodies of some *Drosophila* species suggesting a revision of the current OR/GR categories of chemoreceptor classification. In conjunction with genome sequence data (Gardiner et al., in prep.), this data will also be used to investigate any correlations between coding sequence and gene expression divergence. This combined data has the potential to determine the relative roles of structural and expression modifications in generating prezygotic reproductive isolation and to identify which ORs play key roles as candidate “speciation genes”.

Population divergence in the land snal, *Cepaea nemoralis*

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The terrestrial snail *Cepaea nemoralis* is highly polymorphic in directly observable shell characters. The underlying genetics of these shell characters is simple, facilitating the demonstration of local adaptation and disruptive selection at individual loci. Morph frequency data has revealed that particular shell morphs are more prevalent in particular habitats. At some sites in the UK, such population divergence occurs over short distances, in the order of a few hundred metres. This means that such divergent populations of *C. nemoralis* have great potential as natural model systems to study local adaptation. However, there is a lack of molecular data to support the morph frequency data. A genome-wide scan with amplified fragment length polymorphism (AFLP) markers should reveal loci that are highly differentiated between divergent populations of *C. nemoralis*. Highly differentiated loci are indicative of regions of the genome under selection. This technique can help to find the gene(s) involved in local adaptation.

The search for a rhino fingerprint

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Rhinoceros horn is highly sought after for use in decorative and traditional medicine products. Despite receiving legal protection, rhinos continue to be poached and their horns shipped abroad to supply this demand. Enforcement agencies are hampered by difficulties in identifying evidence samples, limiting their ability to investigate and prosecute this illegal activity. Our aim is to develop forensically validated DNA assays to resolve these issues, by identifying the geographic, population and individual origin of evidence samples. The ability to link a suspect to a crime scene (e.g. blood stain on clothing to a particular rhino carcass) provides valuable evidence which could secure a prosecution. Here we present the preliminary results of mitochondrial DNA typing and STR profiling of the southern white rhino, *Ceratotherium simum*.

Comparative functional analysis of ESTs in two plant species with contrasting population sizes
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The Hawaiian endemic genus *Schiedea* is relatively young (~7Mya), and contains over 32 species that have evolved as part of a recent island adaptive radiation. *Schiedea* species have fairly limited distribution and the population sizes are quite small. *Silene latifolia* is from the same family, *Caryophyllaceae*, but this species is fairly widespread and has an effective population size (Ne) of at least a million individuals that vastly exceeds population sizes of *Schiedea* species. Larger population size is expected to result in stronger codon bias in *Silene*, compared to *Schiedea*, which have not been analysed for these two species. Here we report the analysis of 322 and 302 cDNA sequences from *Schiedea globosa* and *Silene latifolia*. A BLAST search was run on the data set and any genes matching another plant species with an e-value of e-10 or better was accepted. Gene functions of the data set were assigned using the Gene Ontology database and functional enrichment identified and compared between the two species. We also report and discuss the extent of codon bias in the two species.

Molecular variation in the Lim3 locus controlling neuron development is associated with Drosophila melanogaster lifespan
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Lim3 is an essential gene coding for RNA polymerase II transcription factor and playing a key role in neuron specification during *Drosophila* development. *Lim3* was previously nominated as a candidate gene affecting *Drosophila* lifespan (Roshina, Pasyukova, 2007). Fifty substitution *D. melanogaster* lines containing natural second chromosomes in homozygous genetic background and significantly differing in lifespan (De Luca et al., 2003) were used to analyze sequence variation in a 2 kb DNA fragment including 5' surrounding (presumably regulatory) region and 5' untranslated region, first exon and first intron of the major Lim3 transcript. 41 polymorphic sites were revealed, including 38 SNPs and 3 indels. Standard parameters, π and θ, were used to characterize molecular variation. Non-uniform distribution of SNPs was observed among different functional regions: the remote 5' region and intron were the most variable, the 5' region adjacent to the gene was considerably less variable, only one SNP was found in 330 bp 5' untranslated region and no SNPs were found in 109 bp exon. After Bonferroni correction for multiple tests, one SNP was significantly associated with variation in lifespan (P=0.0009). This A-T substitution is 512 bp apart from the structural gene, and results in five days difference in life span. Five more SNPs demonstrated significant associations with life span, which did not survive Bonferroni correction. However, three of these SNPs (two are situated in 5' regulatory region and one in 5' untranslated region) form a haplotype significantly associated with lifespan (P=0.0009). Results of formal neutrality tests are discussed in connection with data on association between molecular variation and variation in life span and *Lim3* expression.

Exploring the evolution of transcription factor binding sites
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The evolution of morphology is in large part due to the evolution of elements that regulate gene expression. Transcription factor binding sites represent the simplest and perhaps the commonest of these elements. While many studies have shown binding sites to be maintained by selective constraint, other studies have demonstrated the rapid (and widespread) turnover of sites. This work presents a new computational method to examine whether this site turnover is due to positive selection or other factors.

Evolutionary implications of pollutants on genetic variability of sentinel bioindicator flatfish.
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The use of widespread marine species as bioindicators of pollutants is becoming commonplace in environmental health assessment programs. Flatfish offer an unparalleled opportunity as sentinel bioindicators. Their benthic lifestyle, and thus close proximity to settled pollutants, and ubiquitous nature, renders flatfish ideal organisms in marine monitoring programmes. The European flounder (*Platichthys flesus*) and dab (*Limanda limanda*) are two such key sentinel species routinely used in monitoring programmes across Europe (e.g. Clean Seas Environmental Monitoring Programme, CSEMP). Currently, biomonitoring focuses on studying biochemical responses, disease levels and compensatory mechanisms triggered by pollution at the individual level. The potential long-term evolutionary effects at the population level are less well understood. Recent studies provide increasing evidence of organisms adapting to environmental pollution at the expense of somatic or reproductive growth and disease resistance. It therefore becomes important to assess the factors impacting the evolution of resistance and adaptive variation. Genetic markers, such as microsatellites, allow us to explore the dynamics of population processes, and can be used to detect the potential for local adaptation and infer levels of self-recruitment and connectivity between populations. Microsatellites for both species have been developed. Once stocks have been defined, and interactions between populations resolved, microsatellite markers will be subsequently implemented along side ongoing biomonitoring programmes to compare the genetic composition and dynamics of flatfish populations taken from reference and polluted sites around the UK. Data from biomarkers of environmental health (e.g. levels of disease) will be integrated with population genetic information to examine the spatial and temporal variation in genetic diversity, population structure and disease incidence.

Genetic diversity of sex chromosome vs. autosome loci in *Microbotryum violaceum*
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Although haploid determination of mating compatibility is common among the fungi, morphologically distinct sex chromosomes are extremely rare in this kingdom. *Microbotryum violaceum* (anther smut pathogen of *Caryophyllaceae* plants) is the only known fungal species with size-dimorphic mating-type chromosomes. Studying of sex chromosome in *M. violaceum* gives the unique opportunity to compare sex chromosome evolution in animals, plants and fungi. While degeneration and low genetic diversity of non-recombining sex chromosomes are common features for both animals and plants, DNA polymorphism patterns in fungal sex chromosomes are unknown. We are presenting data on genetic diversity of sex-linked vs. autosomal loci in *M. violaceum*.

Growing up in a complex genetic landscape: Parasitoid morphology is influenced by complex community genetic interactions in a tritrophic system
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Within a community, there are many species existing together and inevitably interactions arise between them. These interactions may be direct between two species, or indirect spanning a number of other species. Furthermore, there is emerging evidence that intraspecific genetic variation and interspecific genotypic interactions significantly influence the nature of community interactions. I used a model system consisting of rhizobacteria, barley, aphids and aphid parasitoids to investigate how genetic variation within a tritrophic system affects a fourth interacting species. I showed that parasitoid wing size is affected by the specific genotype of aphid it was reared in, specific genotype of barley the aphids were growing on and whether or not there were rhizobacteria present in the soil. Moreover, I found that the wing size is actually affected by the interactions between all these factors – it is affected by the specific combination of aphid and barley genotype and presence or absence of rhizobacteria. This is the first study to show that genetically based interactions within a tritrophic system affect additional species.