

## ABSTRACTS FOR POSTER PRESENTATIONS

The presenting author is shown in **underlined bold**.

(S) indicates that the presenting author is a student, and is eligible for the student poster prizes.

### **The Role of the Environment in HGT**

**Hande Acar**, Katharina Poecher & Jonathan Bollback

The rate of adaptation and complexity of adaptive traits under particular conditions can be predicted by the distributions of fitness effects (DFEs) of the transferred genes. Although we anticipate a substantial environmental dependency of fitness effects of genes from well documented studies of antibiotic resistance genes and metabolic enzymes, we lack a systematic study of the environment-dependence of DFEs. Here we addressed this question by measuring the fitness effects of newly transferred genes in six different environments with different types of cellular stress. We found that the DFEs of horizontally transferred genes are highly dependent on the environment, with abundant gene-by-environment interactions. Furthermore, we demonstrated a relationship between average fitness effect of a gene across all environments and its environmental variance, and thus its predictability. Finally, in spite of the fitness effects of genes being highly environment-dependent, we still observe a common shape of DFEs across all tested environments. In general, our study demonstrates the need for more realistic experiments that include fluctuating environments, heterogeneous environments, and spatially structured environments, such as the animal gut or soil.

### **Phenotypic variation among genotypes of an inversion polymorphism defining behavioral ecotypes in Atlantic cod**

**Einar Árnason** & Ubaldo Benitez Hernandez

The Atlantic cod genome has polymorphic inversions on several linkage groups. Two adjacent inversions on linkage group LG01 are associated with behavioral ecotypes, a shallow-water stationary coastal and a deep-water migratory frontal ecotype. Genotypes at the Pan I locus are a proxy for identifying inversion genotypes. Here we study phenotypic variation among inversion genotypes identified by the Pan I locus.

### **Genetic diversity and divergence in the endangered Cape Verde warbler *Acrocephalus* (S)**

**Helena Batalha**

Genetic factors play an important role in the long-term persistence of populations and species, and conservation strategies should take such factors into account. We used neutral molecular markers to assess diversity and divergence between the three remaining island populations of the little-studied Cape Verde warbler *Acrocephalus brevipennis*. Variation at both microsatellite loci and the cytochrome b gene reveal low diversity within the species overall, but considerable divergence among the populations of Santiago,

Fogo and São Nicolau. There is a gradient of genetic diversity with population size, with the smallest and most isolated population of S. Nicolau being the least diverse, and the largest, Santiago, the most diverse. S. Nicolau is also more divergent from Santiago and Fogo than these two are from each other. The Cape Verde warbler diverged from its sister species, the greater swamp warbler *Acrocephalus rufescens*, within the last million years, and the three populations became isolated from one another 165,000-199,000 years ago. There is also evidence of population bottlenecks, especially on S. Nicolau. This population seems to have decreased during the last century, with potential for further decreases and even extinction. We argue that the three populations should be treated as separate management units.

### **Savvy investment in a microbe (S)**

Philip Madgwick, Balint Stewart, [Laurence Belcher](#), Christopher Thompson & Jason Wolf

Investing in cooperation is costly, and the returns are often available to all group members regardless of personal contribution. Why do individuals pay costs of cooperation instead of leeching off the cooperative investments of others? When individuals do cooperate, how much should they invest? We address these questions by deriving and testing the 'Collective Investment' game. Our model predicts that individuals should strategically invest in cooperation according to their stake in the group. Players with low stake should invest little, whilst those with high stake should invest heavily. This leads to dynamics akin to the Prisoner's Dilemma when neither player has sufficient stake to motivate a substantial investment, causing both players to suffer costs of insufficient investment. We test these predictions in the social amoeba *Dictyostelium discoideum*, which collectively builds a stalk to facilitate spore dispersal. Measurements of natural strains match the predicted 'savvy investment' strategy of stake-dependant investment, with players suffering costs of under-investment when in Prisoner's Dilemma conditions. These findings challenge the 'cooperator' or 'defector' paradigm. Instead, we find that all individuals are savvy investors, strategically modulating investment to maximise their fitness returns.

### **Title TBC (S)**

#### **Max Brown**

Hybrid speciation is a phenomenon that occurs widely in plants, yet conclusive examples of how hybrid species establish are lacking, the frequency of hybrid formation is little known and genomic changes from parent to hybrid species over time are poorly understood. Reproductive isolation is paramount but how this is achieved in the wild is debated. The genus *Euphrasia* is being developed as a system to understand some of these processes. *Euphrasia* are a complex group of hemiparasitic plants that occur in the UK. Recent taxonomy has placed them into 21 species, however a history of reticulation, selfing and rampant hybridisation has confused the situation. The species are of two ploidy levels; diploid and tetraploid and rarely, individuals of differing ploidy levels cross to produce hybrid offspring. My research aims to understand the mechanisms, both genetic and ecological, of hybrid speciation in *Euphrasia* in the UK. As *Euphrasia* are parasitic, a potential mechanism by which *Euphrasia* can become reproductively isolated is through host preference. This is being explored through large growth experiments. Whole genome sequencing of hybrid species and parental progenitors will be undertaken to understand hybrid speciation at the genomic level.

## **Shiny, happy, bugs: investigating colour variation in an aposematic species**

**Emily Burdfield-Steel**, Scott Fabricant, Kate Umbers, Lizzy Lowe & Mariella Herberstein

Color variation in aposematic (i.e. conspicuous and defended) prey should be suppressed by frequency-based selection by predators. Despite this many aposematic species show considerable colour variation. The Hibiscus Harlequin Bug (*Tectocoris diophthalmus*) has a contrasting pattern made up of orange colouration and iridescent blue patches that vary considerably in size between individuals and populations. Furthermore this variation has been shown to influence survival against different types of predators. Here we investigate the causes of colour variation in this species. Using surveys of populations across the species range in Australia, we show that the size of the blue patches varies with both temperature and humidity, and that temperature during development affects the production of the blue, iridescent colouration. However, populations still showed consistent difference in colour even when temperature was accounted for, and different populations showed different levels of plasticity with respect to temperature. Therefore we plan to use Diversity Arrays Technology sequences (DARTseq) to investigate both genetic differences between populations and identify candidate loci that may be involved in colour production.

## **Using locally adapted wild *Brassica* species to identify genes responsible for adaptation to high salinity environments**

**Silvia Busoms**, Charlotte Poschenrieder, David E Salt, Levi Yant

Environmental stresses such as soil salinity are major constraints on plant growth, causing losses in crops around the world. Plant adaptation to salinity stress involves many physiological traits and molecular networks. Thus, the genomic resources available for *Arabidopsis thaliana* and other outcrossing *Brassica* species makes them well suited for the rapid molecular dissection of evolutionary mechanisms in both the context of selfing and outcrossing species. Moreover, many salt-responsive genes have been identified and characterized using transcriptomic and genomic approaches. We find that selective pressures sometimes drive adaptive variants to fixation within demes, but sometimes this is incomplete, for example in cases of fluctuating selection in the context of changing conditions. We have good evidence for local adaptation to the coast in wild demes of *A. thaliana* and *Brassica fruticulosa* from Northeast Catalonia where soil salinity is a major selective force and are pursuing the genomic basis of these adaptations. We also have discovered a dynamic potential case of fluctuating selection in *A. thaliana* in response to temporally varying saline stress. Using two models we are taking advantage of natural variation to identify loci selected in response to high salinity conditions. Here we outline several approaches we are using to achieve this goal.

## **Spatial epigenetic variation in *Timema cristinae* (S)**

**Clarissa F. Carvalho**, Romain Villoutreix, Jon Slate & Patrik Nosil

Epigenetic factors can be an important source of phenotypic diversity in a population. For instance, DNA methylation can influence gene and transcriptional regulation, and therefore it can take part in phenotypic plasticity. However, little is known about how methylation varies in wild populations. Here, we investigated the methylation profile in *Timema cristinae* stick insect, depicting how it varies in space, and which forces are shaping its diversity. We test the hypothesis that natural methylation variation is structured in geographical space, searching for correlations between the patterns and environmental factors, and how

much it reflects genetic variation. We used individuals collected from 12 populations differing in geographical distance and environmental characteristics (e.g. host plant and climate). Using data obtained from whole-genome bisulfite sequencing, we verified methylated cytosines account for 14% in CpG context and are distributed genome-wide, particularly enriched in coding regions. We observed methylation levels tend to cluster following mainly geographical distribution, and that genetic effect significantly explains methylation variation using binomial mixed models. Our results suggest some heritability of the methylation markers, and that changes accumulate given limited dispersal in space. More analyses are necessary to understand the role of environmental factors characterizing the observed patterns.

### **Structure of genotype-phenotype map affects evolvability of a population (S)**

**Jobran Chebib** & Frédéric Guillaume

Phenotypic traits do not always respond to selection independently from each other and often show correlated responses to selection. The structure of a genotype-phenotype map (GP map) determines trait covariation, which involves variation in the degree and strength of the pleiotropic effects of the underlying genes. It is still unclear, and debated, how much of that structure can be deduced from variational properties of quantitative traits that are inferred from their genetic (co)variance matrix (G-matrix). Here we aim to clarify how the extent of pleiotropy and the correlation among the pleiotropic effects of mutations differentially affect the structure of a G-matrix and our ability to detect genetic constraints from its eigen decomposition. We show that the eigenvectors of a G-matrix can be predictive of evolutionary constraints when they map to underlying pleiotropic modules with correlated mutational effects. Without mutational correlation, evolutionary constraints caused by the fitness costs associated with increased pleiotropy are harder to infer from evolutionary metrics based on a G-matrix's geometric properties because uncorrelated pleiotropic effects do not affect traits' genetic correlations.

### **Genome-wide differentiation and adaptation of Atlantic cod ecotypes in the Gulf of Maine**

**Gemma V. Clucas**, L. Kerr, G. Sherwood, S. Cadrin, Douglas Zemeckis, D. Goethel, Z. Whitener & A.I. Kovach

Atlantic cod populations in U.S. waters are presently critically depleted, affecting both the fishing industry and jeopardising genetic diversity and stock resiliency. Preliminary research into the stock composition in the Gulf of Maine suggests there are two sympatrically breeding stocks, which spawn in the same inshore bays, but are differentiated by spawning season and possibly life-history strategy. Prior tagging and morphometric studies suggest the winter- and spring-spawning subpopulations may differ in movement patterns and migratory life-style. Here we investigated the extent of genomic divergence between cod populations in the Gulf of Maine, and whether spawning at different times of the year acts as a barrier to gene flow. Using Restriction Site-associated DNA Sequencing (RAD Seq), we generated a genome-wide set of single nucleotide polymorphisms (SNPs) mapped to the Atlantic cod (*gadMor2*) reference genome and estimated gene flow among populations. We further identified those SNPs putatively under selection. We discuss our findings in terms of genomic pathways involved in the divergence of cod ecotypes in the Gulf of Maine.

### **Genome re-sequencing reveals patterns of local and continental population structure in the unicellular green alga *Chlamydomonas reinhardtii* (S)**

## **Rory Craig**

Despite the importance of *Chlamydomonas reinhardtii* as a model organism for plant genetics and physiology, the population genetics of the species remains largely unstudied. This partly stems from the difficulty of obtaining natural isolates without extensive population structure, as well as the lack of a genome for any outgroup species. In light of this, we have generated population resequencing data for 20 *C. reinhardtii* natural isolates from Quebec, and we have investigated patterns of population differentiation between these novel isolates and all previously sampled individuals from North America. We have also produced a long-read de novo genome assembly for the most closely related known species, *Chlamydomonas incerta*, enabling comparative analyses. Using these resources to estimate nucleotide diversity and divergence, we are investigating the nature of selection acting on different classes of coding and noncoding sequence in *C. reinhardtii*. We are especially interested in quantifying genomic variation in selective constraint, and estimating the proportion of the genome that is evolving under purifying selection.

## **Short term advantage of sexual reproduction under natural selection in finite populations**

### **Daniel J M Crouch**

The prevalence of sexual reproduction remains mysterious, as it poses clear evolutionary drawbacks compared to reproducing asexually. Several possible explanations exist, with one of the most likely being that finite population size causes linkage disequilibria to randomly generate and impede the progress of natural selection, and that these are eroded by recombination via sexual reproduction. For an arbitrary number of loci, the expected change in mean fitness between consecutive generations, a measure of short-term evolutionary success, is shown under random environmental influences to be related to the autocovariance in mean fitness between the generations, capturing the effects of stochastic forces such as genetic drift. Interaction between genetic drift and natural selection, due to randomly generated linkage disequilibria, is demonstrated to be one possible source of mean fitness autocovariance. This suggests a possible role for sexual reproduction in reducing the negative effects of genetic drift, thereby improving the short-term efficacy of natural selection.

## **Genetic diversity in wild and domesticated stands of Norway spruce (S)**

### **Helena Dahlberg & Pär K. Ingvarsson**

Genetic diversity is maintained through the combined processes of mutation, gene flow, genetic drift and selection. Forest tree breeding is a relatively new phenomenon compared to many other crops and the material that is being deployed is, genetically, often very similar to wild-growing populations. It remains unknown to what degree improved seedlings differ genetically from native populations in the surrounding forest and how gene flow from planted areas into native stands alter standing levels of genetic variation. It is also unknown how different forestry practices affect patterns of genetic diversity within and among forest stands. To gain knowledge in this area we will review what is currently known about genetic diversity in managed and natural forest stands and then expand on this by genotyping material sampled from pristine forest stands in northern Sweden to create a baseline of genetic diversity in Norway spruce. Our goal is to evaluate if and how stands planted with genetically improved material differ from naturally re-generated stands in pristine forests.

## **Likelihood-free inference of natural selection and genetic recombination from temporal changes in allele frequencies: Selection strength inferences via Approximation Bayesian Computation framework (S)**

**Xiaoyang Dai**

## **Constructing a linkage map for Swiss Alpine whitefish (S)**

**Rishi De-Kayne**, Ole Seehausen & Philine Feulner

Knowledge about genomic differentiation between species within an adaptive radiation contributes to a better understanding of the role of ecological speciation in creating biodiversity. The recent origin and repeated diversification of fish in post-glacial lakes provides an ideal system in which to study the genomic changes underpinning ecological diversification. Within the Alpine whitefish (*Coregonus* spp.) species complex, the radiations of six or more sympatric species of whitefish in some lakes are thought to have been facilitated by ecological and reproductive strategy differentiation with sympatric species varying in diet, body length, gill-raker number and spawning depth. The first step towards building genomic resources to better understand genomic changes underpinning speciation in this system involves the production of a linkage map. We produced F1 offspring by crossing two wild whitefish from Lake Thun in Switzerland. Both parents and over 120 offspring were genotyped using a RAD approach, resulting in a male and a female linkage map each with ~900 SNP markers. I will describe the structure of the linkage map and the identified synteny of genomic regions between whitefish and other salmonid species.

## **Analysis of spatial genetic variation reveals genetic divergence among populations of *Primula veris* associated to contrasting habitats (S)**

**Pablo Deschepper**, Rein Brys, Miguel A. Fortuna & Hans Jacquemyn

Genetic divergence by environment is a process whereby selection causes the formation of gene flow barriers between populations adapting to contrasting environments and is often considered to be the onset of speciation. Nevertheless, the extent to which genetic differentiation by environment on small spatial scales can be detected by means of neutral markers is still subject to debate. Previous research on the perennial herb *Primula veris* has shown that plants from grassland and forest habitats showed pronounced differences in phenology and flower morphology, suggesting limited gene flow between habitats. To test this hypothesis, we sampled 33 populations of *P. veris* consisting of forest and grassland patches and used clustering techniques and network analyses to identify sets of populations that are more connected to each other than to other sets of populations and estimated the timing of divergence. Our results showed that spatial genetic variation had a significantly modular structure and consisted of four well-defined modules that almost perfectly coincided with habitat features. Genetic divergence was estimated to have occurred about 114 generations ago, coinciding with historic major changes in the landscape. Overall, these results illustrate how populations adapting to different environments become structured genetically within landscapes on small spatial scales.

## **Genome structure and gene content evolution in the Leishmania parasite Viannia subgenus**

**Tim Downing**, Simone Coughlan, Eoghan Feane, Ali Taylor, Mandy Sanders, Gabriele Schonian & James A. Cotton

The genomes of emerging pathogens provide insights into their origin, adaptation and mixing. The unicellular protozoan parasite *Leishmania* causes the neglected tropical disease leishmaniasis. In the Viannia subgenus, so far only *L. braziliensis* and *L. panamensis* have been assembled as reference genomes. Here, *L. naiffi* and *L. guyanensis* were genome-sequenced to assemble and annotate two references. Phylogenetic and evolutionary comparisons of *L. guyanensis* and *L. naiffi* with ten other Viannia genomes revealed four traits common to all Viannia: mosaic aneuploidy, 22 orthologous groups of genes absent in other *Leishmania*, elevated TATE transposon copies, and an amplification of a NADH-dependent fumarate reductase gene. We discovered 70 additional genes not annotated on the original *L. braziliensis* reference. There were limited structural changes in genome architecture specific to individual Viannia species: although most had an unstable ~45 Kb amplification on chromosome 34, common lab isolate *L. shawi* M8408 had a minichromosome on this chromosome, and *L. naiffi* had amplified virulence factor genes. Combining genome assembly with phylogenetics and comparative bioinformatics across an extended panel of diverse Viannia uncovered new insights into the origin and evolution of this subgenus that can help improve reservoir tracking and diagnostics for leishmaniasis surveillance.

### **Global phylogeny of a fragmented finch species (S)**

**Jamie Dunning**, Angus Davison & Kate Durrant

Twite, *Linaria flavirostris*, have a disjunct global distribution- with two isolated groups- one in Asia and one in Western Europe. We use mitochondrial DNA and Colour ring records to measure affiliations between fragmented groups.

### **The causes of genetic variation in susceptibility to infectious disease in natural populations**

**Elizabeth Duxbury**, Ben Longdon & Francis Jiggins

There is abundant genetic variation in susceptibility to infectious disease in animal populations, but the reasons why this variation is maintained are poorly understood. We tested whether selection by parasites, during host-parasite coevolution, increases variation in susceptibility, by comparing patterns of genetic variation across several species of *Drosophila* that are infected either with RNA sigma viruses with which they have coevolved or viruses that normally infect other species. To do this we took full-sib families, infected them with the sigma viruses, and then measured viral titres by quantitative PCR. I present exciting results from these quantitative genetics experiments. The work ultimately contributes to determining how host-parasite co-evolutionary dynamics can alter genetic variation in disease susceptibility, the genetic basis of resistance and the potential for rapid evolutionary change.

### **Experimental adaptation and speciation in rotifers**

**Isobel Eyres**, Afrika Gomez, David Mark-Welch, Manuel Serra, Rhonda Snook, Andrew Beckerman & Roger Butlin

Theory says that gene flow and recombination generally impede speciation (with some exceptions, such as reinforcement). Gene flow and recombination will also impact on the genetic architecture underlying divergent adaptation and barriers to gene exchange, and so on the landscape of genomic divergence. However, these predictions are difficult to test in natural systems because of the need to infer the demographic history and the history of selection simultaneously. Monogonont rotifers, facultatively sexual microscopic metazoans, provide a powerful model for examining these processes using experimental evolution. In a yearlong experiment (~180 generations) we will expose paired populations of rotifers to divergent environments: one high salinity with large algae and one low salinity with small algae. We will manipulate the amount of (a) gene flow between populations and (b) sex within populations, and examine the effect of these on local adaptation, reproductive isolation, and the genomic architecture of divergence. Our experimental approach will complement theoretical and observational approaches, enabling us to answer questions such as how local adaptation evolves in the face of gene flow, how reproductive isolation evolves once local adaptation is in place, how recombination influences these processes, and what signatures can be left in the genome.

### **Is haplodiploidy superior to diplodiploidy? (S)**

**Kirsten M. Farncombe**, Natasha Kensington & Louise J. Johnson

There is a bias towards the prevalence of diploidy in many organisms, with nearly all metazoan taxa undergoing somatic development in this state (Mable & Otto, 1998). Diploidy has the advantage of masking deleterious recessive mutations, as well as providing more opportunity for advantageous mutations. In comparison, mutations are immediately exposed and removed in haploids, therefore offspring will have fewer mutations and higher fitness. Consequently, it was hypothesised that haploids and haplodiploids will diverge faster than diploids in the presence of beneficial mutations, and divergence will be reduced when exposed to deleterious mutations (Crozier, 2008; Otto & Gerstein, 2008). Using Perl simulations (Schwartz, Foy & Phoenix, 2017) three mating systems were compared: haplodiploidy, diplodiploidy, and haplonty with recombination (life cycle is haploid with a brief diploid zygote phase). This was conducted to compare evolutionary consequences of different mating systems, considering variation in sex ratio, population size, and the selective effect and dominance relationship of new mutant alleles.

### **Post-mating pre-zygotic reproductive isolation in pea aphids**

**Varvara Fazalova**, Bruno Nevado, Ailsa McLean & Charles Godfray

We aim to understand which reproductive isolation barriers are required to cease gene flow between emerging species. We focus on pea aphids, *Acyrtosiphon pisum*, which feed on legumes and form multiple races, each adapted to a particular legume host plant. Two reproductive isolation barriers separate the host races: habitat choice and post-zygotic isolation. As reproductive isolation is not absolute for majority of the host races, we predicted that distantly related host races might be separated by additional pre-zygotic reproductive barrier(s). To test this hypothesis, we observed mating behaviour and egg fertilization rates for three types of crosses: among individuals of the same host race, between closely related host races, and between distantly related host races. We did not find significant differences in mating behaviour among three types of crosses. However, we observed drastic reduction in the number of fertilized eggs for the crosses between distantly related host races. Our results suggest that post-mating pre-zygotic reproductive isolation is able to cease gene flow and complete speciation in the pea aphid species complex.

## **Sexual healing**

**Susana Freitas**, Chloe Larose, Darren Parker & Tanja Schwander

Asexual reproduction presents much more reproductive potential than sexual reproduction: it has a demographic advantage, avoids most costs related to mating, and can maintain favourable combination of alleles. All this considered, why isn't asexual reproduction more common in animals? Here we test the prediction that asexual populations are rare because they are associated with a lower rate of adaptation, in comparison with sexual populations. Ever-changing environments favour different combinations of alleles over time, and consequently sex. One biotic factor that is able to promote rapid environmental changes is parasite pressure. Indeed, the "parasite hypothesis for sex" (or the "Red Queen effect") is one of the most widely accepted hypothesis to explain the rarity of asexual reproduction in nature. To test the "parasite hypothesis for sex" we focus on the point of action of host-parasite interactions, the immune defense genes (IG). We use a genus of stick insects (*Timema*) to analyse the effect of the reproductive mode on the evolutionary rates of IG: if host-parasite dynamics are relevant for the ubiquity of sex in nature, then we expect IG to evolve adaptively at a faster rate than the genomic average, when comparing sexual to asexual organisms.

## **The importance of the host phylogeographic structure in the spatial spread of viruses: *Mastomys natalensis* arenaviruses in Tanzania**

Sophie Gryseels, Stuart J.E. Baird, Benny Borremans, Benny, Rhodes Makundi, Herwig Leirs & **Joëlle Goüy de Bellocq**

Many emerging infections are RNA virus spillovers from animal reservoirs. Estimating geographic extents for reservoirs is central to predicting infection risk. Recent studies suggest associations between RNA viruses and intraspecific host subtaxa occupying different geographic regions, potentially refining risk models. However, such associations are expected due to isolation by distance as well as host-intrinsic barriers to viral spread. Only key circumstances in nature such as contact zones can allow causes of host/virus association to be distinguished. We sample across an east-African contact zone between two subtaxa of the multimammate mouse, *Mastomys natalensis*, in Tanzania. On one side we find *M. natalensis* carries Gairo, on the other Morogoro: arenaviruses closely related to the Lassa fever virus; both viruses are present centrally. Multilocus host molecular taxonomy allows us to demonstrate ongoing host hybridization i.e. both viruses have the opportunity to spread into a new host range, but do not, strongly suggesting host-intrinsic barriers. Such barriers could explain why human cases of another *M. natalensis*-borne arenavirus, Lassa virus, are limited to West Africa.

## **The genetic and developmental basis of male genitalia evolution between *Drosophila* species (S)**

**Joanna FD Hagen**, CC Mendes, KM Tanaka, A Blogg, AP McGregor & MDS Nunes

Although *Drosophila simulans* and *Drosophila mauritiana* diverged only 240 thousand years ago, there are already striking differences in the morphology of the male genitalia. The claspers, which are important for the correct positioning of the male during copulation, are twice as large and carry a third more sensory bristles in *D. mauritiana* than in *D. simulans*. It is likely that this rapid evolution has been facilitated by

sexual selection, but in order to unravel how this rapid morphological evolution has occurred, we sought out the causative loci. QTL and high-resolution introgression mapping of clasper morphology revealed two small candidate regions on the left arm of the third chromosome underlying clasper size divergence between the species. An RNAi screen in *Drosophila melanogaster* and differential gene expression analysis, *in situ* hybridisations and population data of *D.simulans* and *D.mauritiana* has identified six promising candidate genes (maximum), which are either expressed in the developing genitalia or have a role in genitalia development. We are currently using CRISPR/Cas9 to generate reciprocal hemizygotes of our most promising candidate gene Tartan, which contains very few non-synonymous changes between the species. Our study will significantly enhance our understanding of how sexual selection facilitates rapid morphological divergence and species isolation in natural populations.

### **Impacts of climate-driven evolution on plant-soil interactions and ecosystem functioning**

**Christoph Z. Hahn**, George A. Airey, Andrew P. Askew, Jason Fridley, Michael Morecroft, Steve Paterson, Emma Sayer, Carly Stevens & Raj Whitlock

Climate change is expected to affect the biotic environment at all levels from the individual to the ecosystem. The underlying processes governing these responses within ecosystems are known to include evolution, demographic change, plasticity and altered species interactions. However, we know almost nothing about how these processes are integrated to shape community- and ecosystem-level responses. Here, we present a project that aims to bridge this knowledge gap. We will use a unique, long-running climate change experiment at the Buxton Climate Change Impacts Lab (BCCIL), where a natural grassland has been exposed to drought, warming and precipitation treatments for more than 24 years. Previous research at the site has revealed how both the grassland plant community, and the underlying soil microbial community have responded to these chronic climate treatments, and also provide evidence for evolutionary changes in plants. Building on this foundation, our new research aims to understand climate-driven soil microbial evolution at BCCIL and to determine its effects on plant-soil interactions and ecosystem functioning.

### **Variance and heteroplasmy of length variation in mtDNA over a single generation transition in Atlantic cod *Gadus morhua***

**Katrín Halldórsdóttir** & Einar Árnason

Length variation is found in Atlantic cod mtDNA. In cod this is based on 40 base pair tandem repeats in the D-loop region of the mtDNA. The tandem repeats are at the 5' end of the D-loop and they can form stable secondary structures. Every cod is heteroplasmic for length variation varying between one and ten repeats. Here we investigate the length variation in a single generation transition from mother to offspring. DNA was PCR amplified from a number of unfertilized eggs from six females. The mean number of tandem repeats among eggs varied as a function of the mean number of repeats among females. However, the eggs of female with a low number of repeats tended to have a higher number than the mother whereas eggs of mother with a high number of repeats tended to have fewer numbers of repeats than the female, a form of regression towards the mean number of tandem repeats. The variance of the distribution of tandem repeats of the eggs of each female are greater than the variance of the female. We discuss the results as mutation by replication slippage and possibility of selection for optimum length.

## **Effects of the ordering of natural selection and population regulation mechanisms on Wright-Fisher models**

**Zhangyi He**, Mark Beaumont & Feng Yu

We explore the effect of different mechanisms of natural selection on the evolution of populations for one- and two-locus systems. We compare the effect of viability and fecundity selection in the context of the Wright-Fisher model with selection under the assumption of multiplicative fitness. We show that these two modes of natural selection correspond to different orderings of the processes of population regulation and natural selection in the Wright-Fisher model. We find that under the Wright-Fisher model these two different orderings can affect the distribution of trajectories of haplotype frequencies evolving with genetic recombination. However, the difference in the distribution of trajectories is only appreciable when the population is in significant linkage disequilibrium. We find that as linkage disequilibrium decays the trajectories for the two different models rapidly become indistinguishable. We discuss the significance of these findings in terms of biological examples of viability and fecundity selection and speculate that the effect may be significant when factors such as gene migration maintain a degree of linkage disequilibrium.

## **Probing the developmental regulation of *Heliconius* wing patterns (S)**

**Laura Hebberecht** López, W. Owen McMillan & Chris D. Jiggins

ATAC-seq (Assay for Transposase-Accessible Chromatin using Sequencing) is an emerging tool to interrogate genomes about the accessibility of their regulatory regions to transcriptional machinery. We are applying it to ask how regulatory landscapes differ between wing sections, morphs and species in a genus of neotropical butterflies. By comparing it to parallel RNA-seq data, we are shedding light on the coordination of wing pattern development, and improving our understanding of the role that cis-regulation plays in generating adaptive novelty.

## **Investigating the Role of Human Colonisation on Population Decline in Madagascar's Highland Flora**

**Andrew J. Helmstetter**, Wolf L. Eiserhardt, William J. Baker, Franck Rakotonasolo, Romer Rabarijaona, Stuart Cable & Alexander S.T. Papadopoulos

Madagascar is home to a large number of endemics, many of which occupy extremely restricted ranges and are classified as near threatened, vulnerable or endangered. The flora of Madagascar is thought to have undergone drastic change since humans arrived on the island. However, the extent to which humans are responsible for population declines in plants is unclear. There is little evidence to suggest whether rare species have always been rare or whether increased extinction risk can be attributed to factors such as habitat loss, long generation times and the extinction of seed dispersers. Here, we examined a variety of common and rare species, including those used in traditional medicines or as sources of local timber, to uncover how population size has changed through time. Using double digest restriction site associated DNA (ddRAD) sequencing we generated genomic data for 10 species across seven families. We then used these data to reconstruct a diverse range of demographic histories and identified a number of species with recent declines in population size, which may have coincided with the human colonisation of Madagascar.

## **Divergence in TE activity across the *Drosophila* phylogeny**

**Tom Hill**

## **Diversity and selection of MHC class I genes in Godlewski's bunting (S)**

**Wei Huang**, Boye Liu, Tobias Lenz, Yanyun Zhang, Lu Dong

The major histocompatibility complex (MHC) is a multiple-copy immune gene family that exists in vertebrates. It can recognize antigens and is highly variable. Characterization of MHC genes in different species and investigating the mechanisms which shape MHC diversity is crucially important to understand what contributes to biological diversity. We used NGS methods to genotype the MHC class I genes of 326 Godlewski's buntings (*Emberiza godlewskii*) sampled in the Western mountain area of Beijing from 2014 to 2016. 487 alleles were identified initially, of which 160 alleles were found to be functional, which can be clustered into six supertypes. Compared with other passerine birds, diversity of MHC class I genes in Godlewski's buntings is relatively high. Nine sites are positively selected and three of them have high amino acid polymorphism. These findings can be explained by the action of balancing selection. Phylogenetic analysis also showed that both classical MHC alleles and non-classical alleles exist. Meanwhile, there was no significant difference in either allele frequencies or supertype frequencies between different altitudes, which could be a result of weak or short-term fluctuating selection. In summary, these results provide a framework for subsequent investigation of selection acting on MHC genes in Godlewski's buntings.

## **An alternative approach to estimate contemporary effective population size using linkage disequilibrium information**

**Tin-Yu Hui** & Austin Burt

## **Human endogenous retroviruses and cancer (S)**

**Michal Izydorczyk**

## **Inferring history from the joint SFS of ancient DNA**

**Jack Kamm** & Richard Durbin

Ancient DNA provides a more detailed view of complex demographic history than possible with only modern samples. However, the low coverage of many samples requires careful consideration when combining them with high coverage data. For example, SFS entries for mutations that are private to low-coverage populations will be distorted due to differing rates of variant discovery. We develop an iterative approach to fitting ancient demography from the SFS, using the method momi. We restrict ourselves to SNPs polymorphic within high-coverage samples, and compute a correction factor for not ascertaining within the low-coverage samples. We also use momi to compute  $f_2$ ,  $f_3$ , and  $f_4$  statistics, and use these interpretable statistics to iteratively improve the model. Finally, as we add more populations to our model,

it may become infeasible to compute the full SFS; we then use stochastic gradient methods to fit the model on random subsets of SNPs. Using this approach, we examine the history of several modern and ancient samples across Eurasia, and estimate the strength and timing of a proposed "Basal Eurasian" gene flow event.

### **Polymorphism-aware phylogenetic models and their applications**

Dominik Schrempf, Nicola De Maio & Carolin Kosiol

The increased availability of sequenced genomes both from closely related species and from individuals of the same species, offers a great opportunity to study the speciation and evolutionary history of populations, provided we can properly model the process of sequence evolution using inter and intraspecific data together.

In my group, we have developed a new method called POLymorphisms-aware phylogenetic MOdel (PoMo). It extends any DNA substitution model and additionally accounts for polymorphisms in the present and in the ancestral population by expanding the state space to include polymorphic states. It is a selection-mutation model which separates the mutation process from the fixation process. Thereby, a Moran process is used to model genetic drift. PoMo naturally accounts for incomplete lineage sorting because ancestral populations can be in a polymorphic state.

Our method can accurately and time-efficiently estimate the parameters describing evolutionary patterns for phylogenetic trees of any shape (species trees, population trees, or any combination of those). I will present what can be learned by applying these methods to genome-wide data sites of seven baboon populations about ancestral population history of this species such as new estimates of divergence times and mutation rates.

### **Genetic rescue of maladapted populations (S)**

Rebecca Lewis, Michael Pointer, Lucy Friend, Kris Sales, Ramakrishnan Vasudeva, Joanne Godwin, Matthew J.G. Gage & Lewis G. Spurgin

How species adapt to temperature is an increasingly relevant question due to the growing issue of climate change. We performed a long-term evolution experiment to explore experimentally how populations adapt to increased temperatures- using the red flour beetle *Tribolium castaneum* as a model. We observed consistent evidence of maladaptation in selection lines maintained at elevated temperatures, both in terms of reproduction and survival. We tested the hypothesis that maladaptation occurred as a result of population bottlenecks by performing genetic rescue experiment, in which we increased population size (from 100 to 10 000 individuals per generation) and introduced gene flow over multiple generations. After several generations of these treatments, we have tested the efficacy of these population demographic manipulations on key components of fitness. We discuss our findings in the context of global warming.

### **When the 'invisible hand' leads selfish individuals to act for the good of the group (S)**

Philip G. Madgwick & Jason B. Wolf

Inclusive fitness theory predicts that individuals should maximize the contribution of their genes to future generations by helping relatives who share genes. Thus, despite its benevolent appearance, cooperation between individuals is necessarily a 'selfish' genetic strategy. However under the special conditions of Adam Smith's 'invisible hand', selfish individuals can inadvertently behave in ways that also benefit non-relatives to appear to act 'for the good of the group'. Here, we identify these conditions using a general game theoretic model in which players maximize inclusive fitness by strategically varying their contribution to a public good in response to their stake in the group. We find that the conditions for the appearance of the invisible hand are captured by the 'control rule', which describes the circumstances where stake interacts with selection to give a player the majority share of the group's investment budget. The rule solves the critical stake above which maximization of inclusive fitness reaps a return on investment through increasing the whole group's success.

### **Social plasticity and sexual isolation: How does the social environment affect fruit fly courtship song?**

**Lucas Marie-Orleach**, Nathan W. Bailey, Michael G. Ritchie

Most phenotypic traits are plastic. However, plasticity's effects on evolutionary dynamics are controversial, especially when plasticity is mediated by the social environment. For example, processes of speciation would be very different if the traits mediating sexual isolation are socially plastic or, instead, canalised. Here, we tested the plasticity of courtship song in two species of the *Drosophila melanogaster* subgroup. Male courtship song consists of rapid short pulses, and the inter-pulse interval (IPI) mediates reproductive isolation. First, we found that IPIs are not affected by the social environment encountered prior to mating, however males sang more when they were exposed to social partners (either con- or heterospecific) than when they were isolated. Second, we tested whether memory was involved in this social plasticity by using focal males of memory deficient *D. melanogaster* lines. These males showed a remarkably similar response to the social environment, suggesting that memory is not involved in this social plasticity. Overall, our results suggest that, although male sexual performance is influenced by the social environment, our results illustrate that the key component of courtship in mediating isolation is canalised. This lack of social plasticity may be an adaptation to avoid costly hybridisation when these species coexist.

### **Genomic signatures of adaptation in an island bird (S)**

**Claudia A. Martin**, David S. Richardson, Brent C. Emerson, Claire Armstrong & Lewis G. Spurgin

Identifying ecologically important traits and establishing their genetic basis are central aims in biology, and key to unlocking our understanding of the mechanisms under adaptation. Understanding the mechanistic basis of ecological adaptation is also essential for predicting how populations may respond to climate change. By combining DNA sequencing with in-depth ecological study, it is increasingly becoming possible not only to identify genes under natural selection, but also to identify ecologically important traits, alongside the ecological factors that drive selection. We use Berthelot's pipit (*Anthus berthelotii*), a small passerine endemic to the Canary Islands, Maderian and Selvagens archipelagos, as a model system to examine the genomic basis of ecological adaptation. The replicated, ecologically variable landscapes through which the populations are distributed make this system ideal for studying evolution in the wild. Using whole genome re-sequencing, RAD-Seq and sequence capture we aim to identify which genes are under natural selection among island populations and the biological processes that drive selection. We will then use "genomically-informed" targeted fieldwork to determine the ecological factors driving variation at loci under selection.

## **Genetics of visual mate recognition in *Heliconius* butterflies**

**Richard Merrill**, Chi-Yun Kuo, Matteo Rossi & Alexander Hausmann

Ecological adaptation can result in speciation, and a goal of evolutionary biology is to identify the genetic changes underlying population divergence. The genetics of divergent behaviours, especially those that contribute to reproductive isolation, have not been well characterized. Behaviours, such as assortative mate preferences, are known to evolve rapidly and are important during speciation. *Heliconius* butterflies are well known for their bright warning patterns. Shifts in colour pattern result in behavioural isolation as males show a preference for their own wing pattern over that of closely related species. However, while the genetics of warning pattern are now known in fantastic detail, our understanding of the corresponding behaviours remains limited. Our research aims to identify the causal genes underlying visual mate recognition in *Heliconius* butterflies. We are developing novel methods to efficiently and accurately quantify visual attraction. By combining modern molecular techniques with accurate behavioural data in mapping populations, we hope to identify the genomic regions underlying differences in visual attraction. We are combining this with expression studies with the ultimate goal of providing candidates.

## **Jersey and Guernsey cattle genetics reveal the Viking colonisation of the English Channel Islands**

Daniel Pitt, Filippo Biscarinie & **Pablo Orozco-terWengel**

Jersey and Guernsey cattle are unique breeds of taurine cattle (*Bos taurus*), renowned for their affable predisposition, small body size and hardiness while still producing milk with an exceptionally high butterfat content (~6%). The origin of the Jersey and Guernsey cattle on the British Channel Islands of their namesake is not clear. It has been suggested that these populations are derived from Normand cattle, or that they derive from African cattle breeds imported to those islands. Here we use a dataset of ~30,000 autosomal SNPs genotyped in 80 animals representing Normand, Jersey and Guernsey cattle, and use approximate Bayesian computation (ABC) to characterise their divergence history. Our results suggest that Channel Island cattle breeds separated from Normandy cattle approximately ~1,250 years before present, coinciding with the Viking settlement of those islands. Additional analyses were carried out to identify signatures of selection at a breed level to characterise local adaptation and selective pressures (both artificial and natural).

**Title TBC**

**Alexander Papadopoulos**

**Genetic structure in *Silene dioica* metapopulations: using both autosomal and sex chromosomal microsatellite markers in order to investigate patterns of genetic structure between and within populations and in the two sexes (S)**

**Elisabet Peedu** & Pär K. Ingvarsson

We will use DACP (discriminant analysis of principal components), isolation-by-distance and F statistics to investigate genetic population structure in 18 *Silene dioica* populations growing on islands in the Skeppsviks Archipelago, outside the coast of Umeå, Sweden. Using 14 microsatellite loci, the aim is to see whether population age, successional age (age of patches within the islands), location of islands and sex influences the amount of gene flow occurring in the archipelago and how these different factors affect the genetic population structure.

### **Genomic approaches to understanding the genetic architecture of antler morphology in red deer (S)**

**Lucy Peters**, Jisca Huisman, Josephine M. Pemberton & Susan E. Johnston

A central goal in evolutionary biology is to determine the genetic architecture of phenotypic variation, as this allows us to gain a better understanding of how traits evolve in response to selection. Until recently, researchers have used pedigree data from long-term ecological studies to estimate trait heritability and examine genetic correlations between phenotypes and fitness related traits. Whilst this approach has helped to explain evolutionary change and/or stasis in some cases, it fails to identify genes and genomic regions associated with trait variation, which can elucidate its evolution. Here, we use genomic approaches to better understand the genetic architecture and evolution of a sexually-selected trait, antler morphology, in a wild population of red deer. Red deer stags have substantial genetic variation associated with antler morphology ( $h^2 \sim 0.4$ ), contradicting theoretical predictions that such traits should have low genetic variation. We examined  $\sim 10$  measures of antler morphology from  $>1000$  red deer antlers to determine if these traits are heritable, and how these estimates vary between traditional pedigree and genomic approaches. This work will provide a foundation to understanding the contribution of specific genomic regions to trait variation, and ultimately, how the genetic architecture of these traits covary with individual fitness.

### **X-Y differentiation is lineage-specific in Swiss populations of *Rana temporaria***

**Barret C. Phillips**, Nicolas Rodrigues, Alexandra Jansen van Rensburg & Nicolas Perrin

Sex chromosomes are a common sex determination mechanism, but even closely related species may not have homologous sex chromosomes. Most frogs have sex chromosomes that are homomorphic but which may still show signs of genetic differentiation. In the common frog (*Rana temporaria*), both XX and XY males occur, and the degree of X-Y genetic differentiation varies both between and within populations. We genotyped adult and juvenile samples of *R. temporaria* collected across Switzerland at markers within the candidate sex-determining region and across the rest of the sex chromosome. Two distinct Y lineages are present in Switzerland, which differ in their propensity to be differentiated from the X. Moreover, X-Y differentiation is lineage-specific—it is common in one Y lineage but uncommon in the other. The distribution of the two Y lineages is dictated by geography—one is found on each side of the Alpine ridge bisecting Switzerland, and both lineages are found in samples from possible glacial refugia in Italy. Finally, this distribution pattern is largely congruent with mitochondrial lineage distributions in Switzerland. These results suggest that differences in Y lineage distribution and sex chromosome differentiation may be a consequence of differentiation due to previous geographic isolation within *R. temporaria*.

### **The Pitfalls of Adaptation to the Better Niche (S)**

**Hanja Pisa** & Jitka Polechová

What conditions favour evolution and maintenance of variation has been one of the core questions in both population genetics and ecology. Typically, population dynamics is considered fast enough so that it does not need to be modelled explicitly. Is this really the case? We propose a simple model to investigate a way in which population dynamics can influence evolution. We consider a habitat that consists of two demes with migration between them. The habitat is populated by two different types of individuals; selection occurs in the form of a negative fitness trade-off within the niches. Density-dependent population dynamics and evolutionary dynamics are modelled jointly. As we assume that generations are discrete, density-dependence can be “overcompensating”, creating potentially large fluctuations in the population size. We found that when such fluctuations arise the evolutionary equilibrium is significantly affected by the ecological dynamics. These fluctuations are easily exploited by types immigrating from the more stable environment, even if they are maladapted. As a result, frequency of the type adapted to the “better” niche decreases.

**A genetic approach to conserving the critically endangered Malagasy day-gecko, *Phelsuma antanosy* (S)**

**Michael Pointer**

**The evolution of the social chromosome supergene across fire ant populations**

**Rodrigo Pracana**, Eckart Stolle & Yannick Wurm

There are few empirical studies on the early evolution of restriction of recombination in sex chromosomes and other supergenes. In invasive populations of the fire ant *Solenopsis invicta*, the two variants of a supergene carried by a pair of “social chromosomes” (SB and Sb) determine whether colonies have a single queen or multiple queens. Because of recessive lethality of Sb, this supergene variant is thought to have restricted recombination. We have sequenced the genomes of samples representing several native populations of the fire ant species-complex to test whether all polymorphic populations carry the social chromosome supergene. We explore how gene flow and Hill-Robertson interference may have affected the supergene system, and compare these dynamics with the early evolution of sex chromosomes.

**Neurotranscriptomic divergence between sympatric *Heliconius* species (S)**

**Matteo Rossi**, S. H. Montgomery, W. O. McMillan, R. Papa, C. D. Jiggins & R. M. Merrill

Divergent behaviours are known to be a key source of reproductive and ecological isolation between species. However, we still know little about how genetic changes produce natural variation in behaviour, and how this may relate to the speciation process. *Heliconius melpomene* and *H. cydno* are brightly coloured tropical butterflies that occur in sympatry, and which still hybridize, albeit at very low frequencies. These species differ in warning patterns, which are also used as mate recognition cues by males. Preferences for conspecific females have a strong genetic component and are an important reproductive barrier. We studied differential gene expression in the eyes and mid-brain of *H. melpomene* and *H. cydno*. We analysed genome-wide patterns of transcriptomic divergence across development. We then focused on

QTL peaks associated with male preference behaviours, with the aim of identifying candidate genes whose expression might be associated with differences in behaviour.

## **Genome Assembly and Alignment using Maps-style Visualization (S)**

**Josiah Seaman**

Working with genome sequences can often be like working with a black box. When looking at more than 10kbp, genome browsers mainly visualize gene annotations, not sequence. Here we present a data visualization technique that can put a gigabase scale whole genome sequence on one screen. The visualization technique is based on a google-maps style zoomable canvas that presents the entire genome sequence as a single static image landscape. The program works on draft genomes, and whole genome alignments. It includes the ability to cross-compare gene annotations in aligned genomes. Using LiftOver alignment files, multiple genomes can be laid out like columns on the page of a book. Here the visualization technique is applied to both plant and animal genomes. First, human, chimpanzee, and gorilla genomes sequences are aligned at the nucleotide level and we verify there is no human sequence contamination. Secondly, the assembly process of the Green Ash Tree genome, *Fraxinus pennsylvanica*, is shown. The visualization is used to pick out scaffolding errors and contamination from a bacterial endophyte. This data visualization technique is aimed at making working with genome assemblies more transparent at every stage.

## **Population Genetic Structures of *Armadillidium vulgare* from South Korea using Mitochondrial COI Gene (S)**

**Jiyeong Shin** & Jongwoo Jung

Terrestrial isopods are distributed widely in the world, contains more than 3,600 terrestrial species. Of these, *Armadillidium vulgare* is distributed worldwide and one of the most common species in South Korea. We investigated genetic variation and population genetic structures of this species based on mitochondrial cytochrome oxidase I (COI) sequences. We collected 68 individuals of *A. vulgare* from 9 locations in the South Korea. From the results, we determined 566 of COI sequences, which were composed of 5 haplotypes. Jeung-do population showed higher haplotype diversity than any other populations. But the pairwise  $F_{st}$  estimates were larger when Bonghwa population was compared with the other populations. Which may come from considerable genetic distance between Bonghwa population and other populations. The genetic structure of this species could be due to a high level of gene flow by human activities except Bonghwa population.

## **Demographic patterns and processes in *Timema* stick insects**

Patrik Nosil & Victor Soria-Carrasco

It has been theorized that species range may be limited by maladaptation due to gene flow from the centre of the distribution towards the periphery, eventually converting range edges in demographic sinks. *Timema* is a genus of stick insects endemic to Southwestern North America with an extensive research programme around the genomics of speciation. This abundance of genomic data accumulated during the last years, along with the recent development of sophisticated model-based inference methods provides the opportunity for testing these predictions. We have conducted the first in-depth comparative analysis of the demographic patterns and processes in *Timema*. We have put special emphasis on the inference of geographic variation in temporal changes in population size and gene flow among populations. We discuss the implications of our findings in the context of the impact of centrifugal gene flow on the evolution of species ranges.

## **Evolutionary genetics and demography of population range expansion in two species of British Lepidoptera (S)**

Evelyn Taylor-Cox, Ilik Saccheri, Jane Hill, Jenny Hodgson & David Roy

Climate change places selective pressure on species to adapt to altered environmental conditions and/or to migrate. When combined with habitat fragmentation many species are unable to track the newly available habitat patches, leading to declines in abundance and distribution. However, the ecological and genetic factors that constrain, or promote, range shifts and range expansion are not well understood. This project will use two range-expanding species of British Lepidoptera, the speckled wood butterfly (*Pararge aegeria*) and black arches moth (*Lymantria monacha*), to study this problem. The history of colonisation and establishment will be reconstructed using a combination of genome scan data, abundance records, and suitable habitat maps. The population genetic data will be further utilised to search for evidence of selection and genetic drift associated with the range expansion process. The poster outlines the overall question, associated hypotheses, and experimental design.

## **Genetics of local adaptation and convergent evolution in the Trinidadian guppy *Poecilia reticulata* using new introduction experiments (S)**

**Mijke J. van der Zee**

Guppies (*Poecilia reticulata*) in the Northern Mountain range in Trinidad show clear phenotypic adaptation to low and high predation environments. Males from low predation environments are more colourful, they have larger body sizes at maturation and reproduce less frequently than their counterparts in high predation environments. Despite the extensive evidence of phenotypic convergent evolution in the wild, relatively little is known about the extent of genetic convergent evolution in natural populations. My research aims to investigate genetic convergent evolution and early adaptation to a new environment in wild guppy populations. In 2008 and 2009, fish from a single high predation location were introduced to four replicate low predation locations, two with a closed canopy and two with an open modified canopy. Using whole genome sequencing (WGS) data from the introduced populations, the source population and one naturally colonised low predation population, we will search for signatures of selection across the genome. Investigating patterns of genome-wide selection in the guppy system offers a unique understanding into the mechanisms underlying rapid evolution in wild populations.

## **Population genetics of the lumpfish (*Cyclopterus lumpus*) across the species range (S)**

**Benjamin Whittaker**, Chloe Robinson, Carlos Garcia de Leaniz & Sofia Consuegra

Lumpfish are of growing interest within aquaculture, both for the harvesting of roe and also as cleaner-fish deployed to control parasitic copepods on salmon farms. The industry faces challenges in meeting requirements to close the production cycle for this novel species, and therefore relies on wild populations to generate commercial stock. Little is known regarding the status and composition of lumpfish populations in the wild, though previous work suggests three genetic clusters in the Baltic Sea, East and West Atlantic. As the demand for lumpfish intensifies harvest pressure increases, so does the incentive for international transport of lumpfish to farm cages from which juvenile fish may escape. Such practises could result in the over-exploitation of wild stocks, and unintentional translocation of non-native lumpfish leading to potential genetic introgression with local populations. I investigated the population genetics of lumpfish across the species range, and found strong population structuring and genetic differences between populations. This should be considered in conservation efforts, management policy and aquaculture practise for the species.

## **The Evolving Moran Genealogy (S)**

### **Johannes Wirtz**

I will introduce and examine the Evolving Moran Genealogy. This process is founded upon and extends the classical Moran model by tracking the history of duplication events of the current generation backward in time, generating a genealogy which can be represented by a binary tree and modified in a way that is in accordance with the underlying Moran model. It has intuitive graphical and combinatorial representations and offers a simple way of reversing time. Of particular interest will be how both EMG and its time-reversed dual process change under conditioning on fixation of a certain allele and altered dynamics, such as the introduction of selectively advantageous/disadvantageous alleles. I will also point out possible implications for the analysis of population data.

## **Genomic consequences of gene flow between *Senecio* species on Mount Etna, Sicily (S)**

**Edgar L.Y. Wong**, Bruno Nevado, Owen G. Osborne, Alexander S.T. Papadopulos, Simon J. Hiscock & Dmitry A. Filatov

*Senecio aethnensis* and *Senecio chrysanthemifolius* are sister species inhabiting contrasting environments of high (above 2000m) and low altitude (below 1000m), respectively, on Mount Etna, Sicily. They form a hybrid zone at intermediate altitudes between their respective ranges. Previous work demonstrated that speciation of these *Senecio* species was likely parapatric, with gene flow continuing ever since their divergence around 100-150 thousand years ago, that coincided with the rise of Mount Etna. Despite their recent divergence, some hybrid breakdown was observed in F2 hybrids, indicating that these species have already evolved some degree of postzygotic isolation. The aim of this work is to identify the genes and genomic regions under diversifying selection that may have contributed to ecological speciation of these *Senecio* species. For this purpose, we analysed the altitudinal gradients in allele frequencies at the genes with strongly differential expression in the two species, as well as a set of likely neutral nextRAD markers across the genome. We present the preliminary analyses of these datasets that reveal candidate genes under diversifying selection. Further analysis will allow us to investigate the selective pressures keeping the two species distinct while maintaining a hybrid zone. Overall, this project aims to reveal the evolutionary forces during on-going ecological speciation driven by adaptation to contrasting conditions at high and low altitudes.

## **The effects of GC-biased gene conversion (gBGC) on the study of natural selection: empirical evidence and theoretical modelling**

Henry Barton & **Kai Zeng**

The neutral and recombination-associated process of gBGC has been shown to exist in many organisms. It can lead to the preferential transmission of G/C nucleotides to the descendants of GC/AT heterozygotes, creating a selection-like force favouring G/C over A/T. In an analysis involving data from the great tit and the zebra finch, we found that estimates of  $\alpha$ , the proportion of substitutions fixed by positive selection, dropped from 48% for the great tit and 64% for the zebra finch, when all variants were analysed, to 22% and 53%, respectively, when we only used variants unaffected by gBGC (i.e., changes between A and T and between G and C). Modelling suggests that the higher estimates based on all variants are probably overestimates caused by gBGC. Our model also reveals that gBGC can bias estimates of the distribution of fitness effects (DFE) from polymorphism data, and may create false correlation between measures of the efficacy of selection (e.g.,  $\alpha$  for positive selection) and recombination rate, which could lead us to erroneously conclude that recombination is a modulator of the efficacy of selection. Importantly, in contrast to demography or selection at linked sites, the confounding effects of gBGC cannot be alleviated by first fitting a demographic model to neutral variants. Thus, considering the confounding effects of gBGC is important when making inferences about selection from polymorphism and/or divergence data.

## **Strain variation in gut microbiota**

**Ana Zhu**

The gut microbiota is a complex ecosystem characterized of multiple strains. Persistence, and prevalence of these strains is currently not well understood due to technical problems. Our group has developed a culturing methodologies to unlock the strain diversity of the gut microbiota. My talk will present my work in exploring the strain population using both culturing and whole genome sequencing of the gut microbiota.