2018 Genetics Society / British Society for Genetic Medicine Meeting

Genotype to Phenotype to Fitness

22 – 23 November 2018. Exeter University

Meeting Programme

100 YEARS the geneticssociety 1919 - 2019

BSGM The British Society for Genetic Medicine

Celebrating 100 years of genetics in Edinburgh and the Genetics Society in the UK

13 November, 2019 - 15 November, 2019
Royal College of Physicians, Queen St., Edinburgh

genetics edinburgh 1919 2019

2019 is coincidentally the centenary of both the Genetics Society and the origins of the Roslin Institute and the Institute of Evolutionary Biology, University of Edinburgh. A joint scientific celebratory meeting will be held from 13-15th November 2019, Edinburgh.

www.genetics.org.uk/events/100-years-genetics

INTRODUCTION

On behalf of the Genetics Society we extend a very warm invitation to the 2018 Autumn meeting Genotype to Phenotype to Fitness. The meeting will bring together researchers working with diverse genetic techniques across a multitude of systems, but who are nonetheless connected by a shared passion for understanding adaptive evolution

The meeting will have four themed open sessions over the two days, each featuring 2-3 of our invited speakers together with contributed talks and posters selected from abstracts submitted. In addition to the open sessions there will be an ECR symposium offering opportunities for early career researchers to present in an especially supportive environment.

Session 1 – Genotype to Phenotype

We have an unprecedented array of tools for interrogating the genotype to phenotype map, including epigenetics, but how do genetic differences translate into fitness consequences for individuals or lineages? What insights can we take from genetic studies of lab models, crops, livestock and wild populations?

Session2 – Constraint and Conflict

Phenotypes under selection are frequently not genetically independent, while individual genes can influence fitness through multiple, sometimes antagonistic, trait pathways. this session will focus on the need to think about multivariate phenotypes, and evolutionary trade-offs (e.g. among traits, between sexes) arising from genetic architecture.

Session 3 -Genes in Environments

The fitness consequences of genetically determined phenotypes depend on the environment that they are expressed, in many interesting ways, from classical genotype-by-environment interactions, through to genetic mediation of social and/or ecological processes.

Session 4 – Micro to Macro

Bridging scales of biological organisations is frequently challenging for evolutionary genetics. Do population specific studies studies and microevolutionary perspectives help us understand divergence among populations and species (or vice versa)? What can we learn from studying the genetics of speciation and/or hybridisation?

Karen Lee, John Innes Centre

Learn more about funding at www.genetics.org.uk

Funding opportunities

- Genetics Society one-day meetings
- Meetings with Genetics Society sponsorship
- Genes and Development summer studentships
- Junior scientist grants
- Heredity fieldwork grants
- Sir Kenneth Mather memorial prize
- Training grants to attend international courses or receive training in another research group

These schemes are aimed at financially supporting researchers in areas of genetics

PROGRAMME

Wednesday 21st November 2018

REGISTRATION OPEN FROM 15:00

Thursday 22nd November 2018

09:00 REGISTRATION OPEN
09:30 WELCOME

GENOTYPE TO PHENOTYPE

09:45 **Chris Jiggins**
Signatures of selection at adaptive wing patterning genes in Heliconius butterflies.

10:15 **Alistair McGregor**
Changes in tartan underlie differences in male genital morpohology between Drospohila species.

10:30 **Anne Charmantier**
Urban versus forest ecotypes in great tits: from phenotypic differentiation to population genomics.

11:00 **Frank Chan**
An integrative genomic analysis of the Longshanks selection experiment for longer limbs in mice.

11:15 TEA/COFFEE & POSTERS

11:45 **Andreas Sutter**
What drives and maintains genetic variation in polyandry?

12:00 **Melanie Brien**
Genetics and condition-dependence of structural colour in Heliconius butterflies.

12:15 **Miltos Tsiantis**
The genetic basis for diversification of leaf form: from understanding to reconstructing.

12:45 LUNCH

CONFILCT AND CONSTRAINT

14:00 **Katrina McGuigan**
Investigating causes of bias in the distribution of heritable phenotypic variation.

14:30 **Ben Ashby**
Understanding the role of eco-evolutionary feedbacks in genetic and phenotypic models of antagonistic coevolution.

14:45 **Andrew Pomiankowski**
Sexual conflict explains the extraordinary diversity of mechanisms regulating mitochondrial inheritance.

PROGRAMME

Thursday 22nd November 2018

15:00	**Susan Johnston** Why is genetic variation in individual recombination rate maintained in mammals?
15:30	TEA/COFFEE & POSTERS
16:00	**Bonnie Fraser** Insights from long-read assembled male genome reveals population variation in guppy sex chromosome evolution.
16:15	**Lara Meade** Adaptive maintenance of fertility in the face of meiotic drive.
16:30	**Raphaël Royauté** Genetic architecture of behavioural syndromes in field crickets:adaption or constraint?
16:45	**Ned Dochtermann** Wrightian versus Holey landscapes: implications for multivariate phenotypes and within-population trait covariation.
17:00	**Nina Wedell** Sex, Conflict and Selfish Genes.
17:30	GENETICS SOCIETY ANNUAL GENERAL MEETING
18:00	DRINKS RECEPTION & POSTERS
19:30	GALA DINNER

Friday 23rd November 2018

GENES IN ENVIRONMENTS

09:00	**Edze Westra** The evolutionary ecology of CRISPR-phage interactions.
09:30	**Waldir Berbel-Filho** Two sides of the same coin: epialleles diverge, phenotypes converge.
09:45	**Lewis Spurgin** The genetics and phenotypic consequences of environmental change – insights from a long-term evolution experiment.
10:00	**Eleanor O'Brien** Interacting effects of the abiotic and biotic environment on fitness and evolutionary potential of rainforest Drosophila.
10:15	TEA/COFFEE & POSTERS
11:00	**Mijke van der Zee** Using whole genome sequences of newly introduced populations reveals rapid genetic convergent evolution in guppies.
11:15	**Jonathan Bridle** Whither local adaptation? Testing how patterns of plasticity and environmental variance affect evolutionary rescue in natural populations.

PROGRAMME

11:30 **Patrik Nosil**
Ecological discontinuity drives multi-genic adaptation in cryptic coloration.

12:00 LUNCH

EARLY CAREER RESEARCHERS

13:15 **Robert Griffin**
Environmental effects on G matrices in humans.

13:30 **Filip Ruzicka**
Genome-wide sexually antagonistic polymorphisms reveal longstanding constraints on sexual dimorphism in the fruitfly.

13:45 **Laura Travers**
Why do dietary restricted animals live longer? Testing the evolutionary theories.

14:00 **Elisa Perez Bada**
Early-life conditions and their effect on senescence in European badgers: all's well that ends well?

14:15 **Helena Wells**
A genome wide association study in the UK Biobank cohort identifies a large number of genome-wide significant loci linked to self-reported adult hearing ability.

14:30 TEA/COFFEE & POSTERS

MICRO TO MACRO

15:00 **Matthew Webster**
The genomic basis of local adaptation and speciation: lessons from birds and bees.

15:30 **Aida Andres**
Genetic differentiation among chimpanzee subspecies and adaptations to viral infections.

15:45 **Leslie Turner**
Investigating genetics of hybrid dysfunction using inbred strains derived from natural populations in the house mouse hybrid zone.

16:00 **Walter Salzburger**
Understanding adaptive radiation and explosive diversification through cichlid fish genomics

16:30 CLOSING REMARKS

MEETING INFORMATION

Meeting organisers

Alastair Wilson
(Exeter Universtity)
Kay Boulton
(The Roslin Institute,
University of Edinburgh)
Frank Hailer
(Cardiff University)
Ben Longdon
(Exeter University)
Helena Wells
(King's College London)

Plenary Speakers

GENOTYPE to PHENOTYPE
Chris Jiggins (Cambridge)
Anne Charmantier (CNRS Montpellier, France)
Miltos Tsiantis (Max Planck, Cologne, Germany)

CONFLICT & CONSTRAINT
Katrina McGuigan (Queensland, Australia)
Susan Johnston (Edinburgh)
Nina Wedell (Exeter)

GENES IN ENVIRONMENTS
Edze Westra (Exeter)
Patrik Nosil (Sheffield)

MICRO TO MACRO
Matthew Webster (Uppsala, Sweden)
Walter Salzburger (Basel, Switzerland)

Location

University of Exeter, Streatham campus

Genetics Society Centenary and full committee meetings will be held on Nov 21st prior to the main conference in the Ibrahim Ahmed Room of Reed Hall (14, 6E).

Registration, talks and posters will be held in the Great Hall (1, 6G). The registration desk will be open from 15:00 -17:00 on Nov 21st and then from 08:30 on Nov 22nd. Teas/coffees and buffet lunches will also be served here.

The Gala Dinner will be held in the Woodbridge Restaurant, Reed Hall (14, 6E)

The Forum (3, 6G) is just next to the Great Hall and has shops, cafes, ATM, and break-out space for discussions. A nursing mother's room is available just down the hill in room 115 of the Old Library (7, 8G).

SITE MAP


STOCKER ROAD
NORTH PARK ROAD
JENNINGS DRIVE
THE QUEEN'S DRIVE
POOLE GATE
PRINCE OF WALES ROAD
AREA A
Academic, Administration & Social Buildings
Residences
Footpath
One-way road
Students' Guild
Info at...
Information point
Bus stops
Steps
Student Information Desk
On-road cycle lane (contraflow)
Traffic-free cycle lane
Main Reception
Parking
Disabled parking
Cycle parking
Locked cycle parking
Food and drink
ATM
Showers
Accessible toilets
Baby changing facilities
Disabled ramp access

MEETING INFORMATION

Information for presenters

The meeting will include contributions from researchers working on diverse organisms, in the lab and in the field, and employing a wide array of genetic tools to study evolution. As you prepare your presentation keep in mind that the audience will be correspondingly broad!

Posters - Please prepare a portrait, A0 poster and bring it to registration upon your arrival. We will have poster boards ready for you!

Speakers – Please prepare a 12 minute presentation, to be followed by a 3 minute open Q&A. We ask that you please pay attention to the length of your talk as we will be fairly strict about cutting you off if you overrun! To help us make everything run smoothly, send your presentation in either ppt or pdf format to theteam@genetics.org.uk by Monday 19th November. There will be an AV team on hand at the conference to help with any issues and you will be able to check slides prior to your presentation.

Prizes

We plan to award prizes for the best student/ECR presentations – poster and talk. Please make sure to tell us when you register if you are a student or postdoc and would like to be considered for these. We are also grateful to Oxford University Press for donating one of the prizes.

WiFi

Is available through EDUROAM and/or the University of Exeter's guest network, Instructions for accessing the latter are available here at:
http://as.exeter.ac.uk/media/level1/academicserviceswebsite/it/documents/networks/wireless/UoE_Guest_Instructions.pdf

GENOTYPE TO PHENOTYPE TO FITNESS

Chair: Nina Wedell

01

CHRIS D. JIGGINS

Department of Zoology, University of Cambridge, UK.

Signatures of selection at adaptive wing patterning genes in Heliconius butterflies.

A major undertaking in evolutionary biology is to link genotype to phenotype and understand the evolutionary changes that lead to adaptation and speciation. Here I will give an overview of our work on the brightly coloured Heliconius butterflies. We have studied signatures of selection across wing patterning loci and shown pervasive evidence for selective sweeps, especially at loci with major effects on wing phenotype consistent with strong selection acting on these loci. Furthermore, comparison between populations gives some indication of those populations which have the most recently evolved phenotypes.

Next I will focus on the cortex locus which controls yellow and white patterns. CRISPR analysis indicates multiple functional genes at this locus, and provides novel insight into the action of the cortex gene itself.

In summary, Heliconius butterflies have provided insight into how a small number of loci can underlie dramatic radiation in ecologically relevant phenotypes.

02

ALISTAIR MCGREGOR

Oxford Brookes University, UK. amcgregor@brookes.ac.uk

Changes in tartan underlie differences in male genital morphology between *Drosophila* species

One of the main aims of evolutionary biology is to identify the genetic basis of phenotypic differences between species. The morphology of male external genitalia evolves rapidly between species presumably driven by sexual selection. For example, the anal plates, claspers and posterior lobes exhibit striking differences in size, shape and bristle number and morphology between the males of *Drosophila simulans* clade species, which last shared a common ancestor as recently as 240,000 years ago. However, little is known about the underlying genes and how they have altered the development of these structures. To address this, we have carried out high-resolution introgression mapping of genes underlying clasper and posterior lobe size differences between *D. mauritiana* and *D. simulans*. We mapped several small regions on chromosome III, which confirmed that variation in these traits is highly polygenic, and showed that different loci underlie clasper and posterior lobe differences. Moreover, we identified a region of 177 kb containing only 9 genes that explains approximately 14% of the difference in clasper morphology between these two species.

Expression and functional analyses of these positional candidates revealed that tartan, which encodes a transmembrane leucine-rich repeat protein that regulates cell interactions, is required for the regulation of clasper development and that cis-regulatory changes in this gene contribute to clasper size differences between *D. mauritiana* and *D. simulans*. Therefore, we have identified a new gene underlying clasper development and one of the first loci underlying the evolution of genital diversification among species.

03

ANNE CHARMANTIER

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Urban *versus* forest ecotypes in great tits: from phenotypic differentiation to population genomics

With its conspicuously altered ecological dynamics, the urban environment stands in stark contrast to the natural environment that has been used as research ground for virtually all long-term studies of vertebrates used as cornerstones in evolutionary ecology research. Because of this ecological contrast, it is often assumed that new phenotypes found in cities are the result of an evolutionary response to novel selection. We initiated a comparative study of urban versus forest great tit Parus major populations in 2011, which quickly revealed phenotypic divergence for a large set of morphological, behavioural and life history traits. I will walk you through the steps of our project aiming to test whether this divergence is the result of local adaptation. First, a comparison of reproductive selection in the two habitats failed to support the hypothesis that contemporary selection explains differences in morphology and life history between urban- and forest-breeding great tits. Second, using 70,000 SNPs produced by RAD-sequencing, we investigated the genome wide effects of urbanization on neutral and adaptive genomic diversity in 141 adult great tits collected in locations having different urbanization degrees.

Our results showed low genetic differentiation across the urbanization gradient (Fst between most and least urbanized sites = 0.008), suggesting an absence of strong effect of urbanization on great tit gene flow. Relatedness was however on average higher among individuals found in urbanized zones compared to rural ones, suggesting demographic impacts of urbanization. Genome scans revealed several footprints of divergent selection along the urbanization gradient. These findings open exciting perspectives for broader investigations of genomic bases related to adaptation in urban environment, notably in relation to avian personality and metabolism.

04

FRANK CHAN

Friedrich Miescher Laboratory of the Max Planck Society, Germany. frank.chan@tue.mpg.de

An integrative genomic analysis of the Longshanks selection experiment for longer limbs in mice

Evolutionary studies are often limited by missing data that are critical to understanding the history of selection. Selection experiments, which reproduce rapid evolution under controlled conditions, are excellent tools to study how genomes evolve under strong selection. Here we present a genomic dissection of the Longshanks selection experiment, in which mice were selectively bred over 20 generations for longer tibiae relative to body mass, resulting in 13% longer tibiae in two replicate lines. We synthesized evolutionary theory, genome sequences and molecular genetics to understand the selection response and found that it involved both polygenic adaptation and discrete loci of major effect, with the strongest loci likely to be selected in parallel between replicates. We show that selection may favor de-repression of bone growth through inactivation of two limb enhancers of an inhibitor, Nkx3-2. Our integrative genomic analyses thus show that it is possible to connect individual base-pair changes to the overall selection response.

05

ANDREAS SUTTER

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What drives and maintains genetic variation in polyandry?

What drives mating system variation in nature is a major question in evolutionary biology. Female multiple mating (polyandry) has evolutionary consequences for diverse phenomena from gene expression to population productivity. However, our understanding of the evolution of polyandry is hampered by a bias towards looking at the fitness consequences of limiting females' access to males in species that are naturally highly polyandrous. Hence, what drives and maintains variation in polyandry between individuals, genotypes, and populations within a species remains poorly understood. Polyandry may reflect a syndrome where only females genetically predisposed to multiple mating benefit from polyandry. Alternatively, polyandry may in many species be selectively neutral, and variation in polyandry may arise by chance.

To test these hypotheses, we used isofemale lines of Drosophila pseudoobscura, where variation in polyandry between and within populations is under strong genetic control. In single-generation experiments, we found that multiple versus single mating had no clear fitness effects in terms of fecundity or longevity, irrespective of a female's genetic predisposition to polyandry. Hence, polyandry appeared selectively neutral, and there was no evidence for a polyandry syndrome. Next, we investigated how polyandry evolves in a social context. We set up replicate experimental populations that mimicked situations with either high or low initial levels of polyandry, and tracked female mating behaviour over 7 generations. The frequency of polyandry remained stable over time, matching the initial starting frequencies of the respective experimental populations. Thus, results were consistent with strong genetic control over female remating behaviour. However, there appeared to be no fitness differences between more versus less polyandrous genotypes, and polyandry did not appear to be under balancing selection.

Whether polyandry shows genetic variation within populations deserves exploration in more species. Understanding within-species variation better would improve our understanding of how mating systems evolve.

06

MELANIE BRIEN

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Genetics and condition-dependence of structural colour in Heliconius butterflies

While most colours on butterfly wings are formed by pigments on the scales of the wings, iridescent colour is caused by the interaction of light with structures on the scales. The tropical butterfly Heliconius erato can be found across Central and South America. However, only subspecies found in Ecuador and Colombia show this bright, highly reflective colour.

Little is known about the genetic basis of structural colours. By combining genomic and phenotypic data, we found that iridescence is sex-linked and controlled by multiple loci. We also show that iridescent colour is a condition-dependent trait. We found that pupae which developed in a stressful temperature environment had lower levels of UV reflectance when they emerged as adults. Sexual dimorphism in UV reflectance suggests this trait is used in sexual selection.

07

MILTOS TSIANTIS

Max Planck Institute, Cologne, Germany.

The genetic basis for diversification of leaf form: from understanding to reconstructing

A key challenge in biology is to understand how diversity in organismal form is generated. Genetic analyses in model systems have identified key regulators that sculpt the body plans of metazoa and seed plants. However, less is known about how the action of such regulators produces particular organ shapes, or how the balance of conservation versus divergence of relevant developmental pathways generated the tremendous morphological diversity of multicellular eukaryotes. One impediment to answering these questions is the relative paucity of experimental platforms where morphogenesis and its evolution can be studied in depth and in an unbiased fashion.

To circumvent this problem, we developed the *Arabidopsis* thaliana relative *Cardamine hirsuta* into a versatile system for studying morphological evolution. We use a combination of genetics, advanced imaging and computational modelling to understand the molecular mechanisms through which leaf morphology evolved in these species, resulting in simple, undivided leaves in *A. thaliana* and dissected leaves with distinct leaflets in *C. hirsuta*.

This presentation will discuss our progress towards understanding the developmental pathways that specify dissected versus entire leaf shapes and that regulate the number, position and timing of leaflet production. It will also detail how studies in *C. hirsuta* have helped understand to what degree pathways underlying morphological variation between and within species overlap.

CONFLICT AND CONSTRAINT

Chair: Chris Jiggins

08

KATRINA MCGUIGAN

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Investigating causes of bias in the distribution of heritable phenotypic variation

The joint distribution of effects of alleles on both traits of interest and on fitness will determine whether mean of the trait evolves. These distributions are not well understood, but some evidence suggests biased directional effects on individual traits, or in multivariate phenotypes. Drawing on data from mutagenesis experiments in the zebrafish we investigated whether mutation load altered the population mean value for traits including size and swimming performance.

Results highlight variability in age-dependency of phenotypes, and suggest the potential for directionally biased mutational effects on timings across the life cycle to bias the distribution of phenotypes available to selection.

09

BEN ASHBY

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Understanding the role of eco-evolutionary feedbacks in genetic and phenotypic models of antagonistic coevolution

It is widely recognised that eco-evolutionary feedbacks can have important implications for evolution, yet theoretical models – especially those with more complex genetics – often ignore ecological dynamics for the sake of simplicity and/or tractability. There are many difficulties in fully reconciling this approach with eco-evolutionary models, and as such the precise role of ecology in shaping evolutionary outcomes is often poorly understood. Here, I will discuss a novel method for introducing eco-evolutionary feedbacks into genetic and phenotypic models to test their predictions under more realistic conditions.

Crucially, this approach: (1) allows the strength of eco-evolutionary feedbacks to be independently varied to determine how and when population dynamics are likely to affect the outcome; and (2) is straightforward to implement so that it can be readily adapted to a wide range of evolutionary models.

Applying this approach to simple examples from the literature on antagonistic coevolution, I show that the inclusion of eco-evolutionary feedbacks often drastically changes the results, for example causing shifts between monomorphism, polymorphism, and fluctuating selection.

10

ANDREW POMIANKOWSKI

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Sexual conflict explains the extraordinary diversity of mechanisms regulating mitochondrial inheritance

Mitochondria are predominantly inherited from the maternal gamete, even in unicellular organisms. The mechanisms enforcing uniparental inheritance are highly diverse and may act either at/after fertilization (maternal control) or during spermatogenesis (paternal control). Using a novel evolutionary model, we show that maternal control favours strict uniparental inheritance with complete exclusion of sperm mitochondria.

Whereas some degree of paternal leakage of mitochondria is expected under paternal control. This difference arises because genetic linkage between mitochondria and nuclear genes builds up with maternal control but declines under paternal control.

Sexual conflict is an inevitable outcome and is a reason for the repeated evolution of novel mechanisms that regulate the transmission of mitochondria. Our analysis suggests that the widespread occurrence of paternal leakage and prevalence of heteroplasmy are also natural outcomes of this conflict.

11

SUSAN E. JOHNSTON

University of Edinburgh, UK.

Why is genetic variation in individual recombination rate maintained in mammals?

Recombination is a fundamental feature of sexual reproduction, ensuring proper disjunction, preventing mutation accumulation and generating new allelic combinations upon which selection can act. However it is also mutagenic, and breaks up favourable allelic combinations previously built up by selection. These trade-offs were thought to tightly constrain recombination rates, but recent genomic studies have shown that individual rates are variable, heritable and have an oligogenic architecture. This implies that recombination rate itself has the potential to evolve rapidly and impact the speed at which populations respond to selection.

Recent genetic mapping studies in mammals have shown that variation in recombination rate has a relatively conserved oligogenic architecture in mammals, with large, often sexually dimorphic allelic effects on individual crossover rates. Interestingly, genetic variation appears to be maintained at relatively common allele frequencies, particularly at genomic regions containing RNF212 and RNF212/REC8. However, there remains little understanding of the selective mechanisms by which this variation is maintained.

We use pedigree and high density SNP information from wild populations of Soay sheep and red deer to determine individual crossover rates, identify genomic regions underpinning recombination rate variation, and their associations with individual fitness over 30+ year periods. Ultimately, this research sheds light on the mechanisms by which genetic variation at recombination rate loci is maintained i.e. through contemporary fitness trade-offs and/or potentially through historical balancing selection.

12

BONNIE FRASER

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Insights from long-read assembled male genome reveals population variation in guppy sex chromosome evolution

Fish show enormous variation in sex determination pathways, allowing us to test theories of sexual conflict and early sex chromosome evolution. When a sex determining locus (SDL) is first recruited to a new autosome, the surrounding region typically shows a reduction in recombination, which will eventually lead to the evolution of distinguishable, non-recombining sex chromosomes. A major hypothesis for this process is that the SDL becomes linked to genes with sex-specific fitness effects, as this helps resolve sexual conflict. The Trinidadian guppy is often cited as an example of sex-linked male advantageous loci. Early studies showed that many male pigment traits were Y-linked, particularly in high predation environments where sexual conflict acting on pigmentation is strongest, suggesting that reduced recombination could evolve quickly and repeatedly.

Unfortunately, the genomic data supporting this hypothesis has been equivocal, with population genomics data suggesting the opposite pattern of reduced recombination in LP populations and disagreement concerning the placement and size of the Y non-recombining region. One major disadvantage of these studies is the lack of a male reference genome in which the non-recombining part of the Y chromosome is reliably assembled.

Here we present a male guppy reference genome made with long read (PACbio) and chromosome contact (HiC) data. By combining state-of-the-art structural genomics approaches with population genomics and ecological data, we are using this resource to identify the male specific region in multiple high and low predation populations.

13

LARA MEADE

University College, London, UK. lara.meade.13@ucl.ac.uk

Adaptive maintenance of fertility in the face of meiotic drive

Meiotic drive genes gain a transmission advantage through the manipulation of meiosis and destruction of non-carrier sperm. Gamete loss is expected to have grave implications for male fertility. In several species this has selected for adaptive suppression of drive in males, and female avoidance of fertilization by drive males through mate choice and polyandry.

Here we report a novel adaptation to X-linked SR meiotic drive in the Malaysian stalk-eyed fly, *Teleopsis dalmanni*. Contrary to other systems, we find that drive males do not suffer fertility loss. They deliver as many sperm per mating as wildtype males, even when they mate multiply. This sperm allocation strategy is possible as drive males have greatly enlarged testes which compensate for the destruction of half their sperm.

But there are also overt costs of drive. Drive males reduce allocation of resources to accessory glands, leading to slow re-mating and a lower mating rate. Body size and eyespan are also reduced, which impair male attractiveness to females. Our study challenges conventional assumptions about adaptive responses to drive, such as genetic suppression, female choice and polyandry, which reduce the equilibrium frequency of drive. Increased investment in sperm production and maintenance of fertility have the opposite effect, enhancing spread and driving up element frequency. This may explain the evolutionary persistence of drive in the *Teleopsis* stalk-eyed fly clade.

14

RAPHAËL ROYAUTÉ

North Dakota State University, USA. raphael.royaute@gmail.com

Genetic architecture of behavioural syndromes in field crickets: adaptation or constraint?

Genetic correlations have the potential to impose constraints on the evolution of populations. These potential constraints have been shown to be greater for behavioural traits versus either life-history or physiological traits. However, the long-term evolutionary consequences of behavioural syndromes depend on whether such correlations originate from pleiotropy or selection-induced linkage disequilibrium. Correlations due to pleiotropy are expected to be more stable and impose longer-lasting constraints on evolutionary trajectories than those originating from drift or linkage disequilibrium.

Using field crickets (Gryllus integer), we compared the architecture of behavioural traits at the phenotypic and genetic level among five geographically separated populations. Using a full-sib, half-sib breeding design, we recorded the activity, antipredator response, and boldness of 788 crickets from the five different populations.

We detected the presence of an activity-antipredator response syndrome at the genetic level in two populations. However, matrix comparisons based on random skewer (all pairwise $r^{\circ} > 0.85$) and geometric subspace analyses (all p-values < 0.05) suggest that multivariate structure among behavioural traits were highly conserved among populations. This result was consistent at both genetic and phenotypic levels, suggesting also that environmental influences similarly affected different populations. Our results provide support for the constraints hypothesis and indicate that pleiotropy may strongly influence a populations' evolutionary responses.

15

NED DOCHTERMANN

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Wrightian versus Holey landscapes: implications for multivariate phenotypes and within-population trait covariation

Understanding why populations typically exhibit considerable variation in traits is a long-standing topic of research in evolutionary biology. Most explanations focus on active processes such as negative frequency dependent selection. However, an alternative explanation is that trait variants—or, rather, suites or syndromes of trait variants—ultimately exhibit similar fitnesses and thus variation remains in populations unless lost through drift or other stochastic processes.

This alternative explanation is consistent with adaptive landscapes that are relatively flat when characterized for a sufficiently high number of traits. While such landscapes may also contain areas of very low fitness, i.e. holes in the landscape due to effectively impermissible trait combinations, the otherwise flat surface allows both population divergence and, simultaneously, the presence of within population multivariate variance. This theoretical possibility can be contrasted with a more classic conceptualization of adaptive landscapes containing optima and a complicated topography of peaks, ridges, and valleys. Classic Wrightian Landscapes and the alternative, Holey Landscapes, have primarily been investigated for their role in speciation but have important implications for within-population variation and the multivariate distribution of phenotypes.

Unfortunately, critical tests vis-à-vis within-population variation distinguishing between these two theoretical constructs are rare within the literature. An important barrier to such testing has been unclear phenotypic predictions for each theoretical construct. Using individual-based simulation models I present predictions about how the within-population multivariate structure is expected to be shaped under either theoretical framework. In brief, Wrightian and Holey landscapes produce different patterns in estimable phenotypic (and genotypic) geometric subspaces: Wrightian landscapes result in linear decreases in the eigenvalues of phenotypic covariance matrices while Holey landscapes produce single-step declines in eigenvalues with one or few dimensions exhibiting appreciable variation.

16

NINA WEDELL

Centre for Ecology & Conservation, Penryn campus, University of Exeter.

Sex, Conflict and Selfish Genes

Selfish Genetic Elements (SGEs) are genes, organelles or microorganisms present within the genome or cell of an organism that spread by subverting normal patterns of inheritance to increase their representation in the next generation; hence the term 'selfish'. SGEs such as endosymbionts, transposable elements, and meiotic drive genes are ubiquitous in living organisms and often associated with fitness costs to the bearer.

Despite their impact on the reproduction of their host, their potential role in sexual selection and sexual conflict is largely overlooked. I will discuss some recent work examining the impact of a variety of SGEs showing they can affect the behaviour and reproduction of their host, often with sex-specific effects, and argue they are important contributors in shaping sexual selection and sexual conflict.

GENES IN ENVIRONMENTS

Chair: Bonnie Fraser

17

EDZE WESTRA

University of Exeter, Penryn Campus, UK. E.R.Westra@exeter.ac.uk

The evolutionary ecology of CRISPR-phage interactions

Bacteria have a range of sophisticated immune mechanisms to protect against virus infections that are favoured under different ecological conditions (1). Under laboratory conditions, bacteria typically evolve de novo virus resistance using either surface modification or CRISPR-Cas adaptive immune systems. In this talk I will discuss how both biotic (unpublished data) and abiotic (2) factors tip the balance in the evolution of these two immune mechanisms, and how this impacts the coexistence and coevolution between bacteria and their phages (3, 4). I will also discuss the impact of sophisticated anti-CRISPR strategies encoded by some phages (5, and unpublished data).

References

1. van Houte S, Buckling A, Westra ER. Evolutionary Ecology of Prokaryotic Immune Mechanisms. 2016 *Microbiol Mol Biol Rev*. 80(3):745-63.
2. Westra ER, van Houte S, Oyesiku-Blakemore S, Makin B, Broniewski JM, Best A, Bondy-Denomy J, Davidson A, Boots M, Buckling A. 2015 Parasite Exposure Drives Selective Evolution of Constitutive versus Inducible Defense. *Curr Biol*. 25(8):1043-9.
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Two sides of the same coin: epialleles diverge, phenotypes converge

Besides considerable research has been proposing different genetic mechanisms to explain genotype-by-environment (G x E) interactions (i.e. epistasis, genetic assimilation), virtually no information is available on how non-genetic mechanisms (epigenetics) interacts with genotypes to generate plastic responses on G x E interactions. Epigenetic modifications may play an important role on local adaptation, however, to fully understand the role of epigenetic on generating plasticity is necessary to detangle genetically-dependent from genetically-independent epigenetic variation. This task has been proven specially challenging due to the genetic variation across individuals.

The present study two highly inbred strains of the self-fertilising mangrove killifish *Kryptolebias marmoratus* to evaluate the distribution of DNA methylation states when different genotypes face similar environments. Individuals were reared for 10 months in individual tanks under two different environments with different degrees of enrichment. Using reduced representation bisulfite sequencing to assess differentially methylated cytosines (DMCs) and regions (DMRs) across genotypes and environments. Additionally, we evaluated genotypes and environment effects on stress-related measures (metabolic rate and cortisol levels). Our results revealed a higher methylation differences between strains than environments, supporting a genotype role on DNA methylation variation.

The commonly affected annotated DMCs and DMRs across genotypes mostly followed a G x E pattern, with similar environmental conditions having contrasting DNA methylation according to the underlying genotype. Few DMCs had similar patterns of methylation variation across genotypes and environments, supporting idea that genetically-independent epialleles may be limited. Despite remarkable epigenetic differences across genotypes, similar stress-related phenotypic responses to similar environmental conditions across genotypes were identified, with no indication G x E interactions, suggesting that epigenetic signatures under G x E interactions could still result into similar phenotypes.

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The genetic and phenotypic consequences of environmental change - insights from a long-term evolution experiment

Measuring genetic and phenotypic change in populations exposed to a novel environment can help us better understand evolutionary adaptation, and may have relevance for understanding the likely impacts of human-induced climate change. I will present results from a long-term evolution experiment in which red flour beetles (Tribolium castaneum) have been exposed to extreme temperature for over 60 generations in the laboratory.

We have found clear evidence for adaptation to high temperature, but this adaptation appears to be incomplete, and sex specific. Whole genome sequencing of the experimental lines suggests that a genome-wide response to increased temperature has occurred, and that identifying specific genes involved in thermal adaptation is likely to be challenging. Nonetheless, experimental evolution will be a powerful tool for understanding genetic and phenotypic consequences of environmental change.

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Interacting effects of the abiotic and biotic environment on fitness and evolutionary potential of rainforest *Drosophila*

Understanding how abiotic and biotic components of the environment determine species' abundance and fitness, and the capacity for species to evolve in response to changes in these components, is critical for understanding what drives species' range limits, and for predicting their resilience to climate change and habitat loss. Using the Australian rainforest specialist *Drosophila birchii*, we conducted field transplant experiments of genetically diverse populations to sites along elevational gradients spanning the climatic range of the species.

We exposed them to varying levels of intraspecific and interspecific (with the co-occurring species *D. bunnanda*) competition to determine: (1) how abiotic and biotic variation interact to drive selection on *D. birchii*, and (2) the potential for rapid evolutionary responses of *D. birchii* to changes in these aspects of the environment. We discovered that abiotic variables and competition both had very large effects on *D. birchii* fitness, and that their relative importance changed across the species' ecological range. Mean fitness declined with increasing competition and elevation, and the negative effect of competition on *D. birchii* fitness was greater at the warm margin of the species' distribution. However, variance in fitness increased in association with increasing competition and elevation, implying that the abiotic and biotic environments will both shape the potential for evolutionary responses to environmental change. Surprisingly, *D. birchii* responded to increasing interspecific, but not intraspecific, competition by producing offspring with a strongly male-biased sex ratio.

This has implications for dispersal and population growth rate where interactions with competing species are most frequent, and may be a key factor shaping species' co-occurrence, and the position of species' range margins.

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21

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Using whole genome sequences of newly introduced populations reveals rapid genetic convergent evolution in guppies

Despite substantial evidence for rapid phenotypic evolution in response to new environments, relatively little is known about the signatures of evolution at the genetic level in these novel situations. Guppies (*Poecilia reticulata*) in the Northern Mountain range in Trinidad show clear repeatable phenotypic adaptation to low and high predation environments. Furthermore, introduction experiments have shown that transplanted guppies evolve a phenotype similar to the naturally colonised low predation populations relatively quickly, in as little as 4 years. Males in introduced populations evolved to be more colourful, have larger body sizes at maturation and reproduce less frequently than their source high-predation environments. How these populations adapted so quickly at the genetic level is unknown.

Using newly introduced populations, my research aims to investigate the genetic architecture of this rapid convergent evolution to a new environment. 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. After 4-5 years (2-3 generations per year) all the populations were sampled in 2013 and subsequently their whole genomes were sequenced.

PCA shows that the introduced populations cluster with their source, showing no evidence of a major bottleneck. Using FST outlier approaches, we scanned the whole genome sequencing (WGS) data from the introduced populations, the source population and one naturally colonised low predation population for signatures of selection. Investigating patterns of genome-wide selection in the guppy system offers a unique understanding into the mechanisms underlying rapid evolution in wild populations.

22

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Whither local adaptation? Testing how patterns of plasticity and environmental variance affect evolutionary rescue in natural populations

The rate of local adaptation along an ecological gradient, and therefore the width of a species' ecological niche, is determined by three main parameters: (1) the rate of change of the environment from the organism's perspective; (2) The strength of local selection and (3) The amount of genetic variation in fitness. However, we lack empirical estimates of all of these parameters under field conditions.

Environmental variance, and the plastic responses of genotypes to this variance, will affect all three of these parameters, and means that laboratory estimates of fitness and genetic variance will fail to predict adaptive responses in the wild. I will present data from our experiments to test the effects of plasticity on evolutionary responses in European butterflies and flowering plants, and in particular how these effects may vary when genotypes experience novel ecological regimes.

23

PATRIK NOSIL

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Ecological discontinuity drives multi-genic adaptation in cryptic coloration

Ecological discontinuities can impose strong selection that helps package polygenic variation into discrete units of diversity, such as morphs, ecotypes, and species. However, direct tests of this hypothesis are lacking. Here we demonstrate that multiple loci affect cryptic coloration in stick insects, but that these loci are found in combinations that generate weakly to strongly discontinuous color morphs.

We use observational and experimental data to show that weak morph differentiation is associated with use of host plants favoring fairly continuous color variation. In contrast, strong morph differentiation is associated with use of hosts favoring very different colors (i.e., green leaves versus brown stems), and structural genomic changes that suppress recombination. Our results show how ecological discontinuities drive polygenic adaptation, involving both strong selection and reduced recombination.

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EARLY-CAREER RESEARCHER SYMPOSIUM

Chair: Susan Johnston

24

ROBERT GRIFFIN

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Environmental effects on G matrices in humans

Environment can mediate genetic (co)variance. Quantitative genetic properties such as heritability, genetic correlations and G matrices may therefore be specific to the environment in which a population is measured.

We use extensive life history data from a recent human population, which was sensitive to environmental variation, to assess the stability of G matrices across environments.

25

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Genome-wide sexually antagonistic polymorphisms reveal longstanding constraints on sexual dimorphism in the fruitfly *Drosophila melanogaster*

Understanding the limits to sex-specific adaptation requires a description of its underlying genetic constraints—i.e., of sexually antagonistic polymorphisms, where different alleles are favoured by selection in each sex. Previous theory has made a number of predictions regarding the identity and functional properties of sexually antagonistic polymorphisms, and their effects on quantitative and population genetic fitness variation. Yet despite this, little is known about the genetics and evolutionary dynamics of antagonistic polymorphisms. To address this, we perform a genome-wide association study of sexual antagonism across ~200 *D. melanogaster* hemiclones.

We identify ~230 independent genetic clusters of antagonistic SNPs. Contrary to classic theory, we find no evidence that these SNPs are preferentially X-linked. Characterising antagonistic SNPs functionally, we find a large excess of missense variants. We also assess the evolutionary persistence of antagonistic variants by examining extant polymorphism in wild *D. melanogaster* populations. Remarkably, antagonistic variants are associated with multiple signatures of balancing selection across the *D. melanogaster* distribution range, indicating widespread and evolutionarily persistent (>10,000 years) genomic constraints. Based on these results, we propose that antagonistic variation accumulates due to constraints on the resolution of sexual conflict over protein coding sequences, thus contributing to the long-term maintenance of heritable fitness variation.

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LAURA TRAVERS

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Why do dietary restricted animals live longer? Testing the evolutionary theories

Dietary restriction (DR) increases lifespan across a broad range of taxa but the evolutionary significance of this phenomenon is still poorly understood. The resource reallocation hypothesis proposes that starved animals are diverting resources from reproduction to somatic maintenance to increase survival in times of nutrient scarcity for the sake of future reproduction. An alternative explanation argues that delaying reproduction in nature is not adaptive. Contrary to classic theory, this "by-product longevity" hypothesis proposes that dietary restricted animals increase nutrient recycling via autophagy and apoptosis to maximise immediate reproduction.

Because increased autophagy reduces cellular toxic waste, it results in longer lifespan as an unselected by-product. Here we explore whether the physiological changes associated with DR are an adaptive response to increase survival or immediate reproduction during famine. The "by-product longevity" hypothesis makes a unique prediction that downregulating autophagy in DR animals will reduce reproduction.

To investigate the effect of autophagy on lifespan and reproduction we used RNA interference to inhibit an autophagic gene bec-1 in the genetic model of DR (eat-2) and in wildtype Caenorhabditis elegans nematodes. Preliminary findings suggest that inhibiting autophagy throughout adult life leads to increased reproduction in both dietary restricted and wildtype worms. We also found that autophagic inhibition results in a shorter lifespan under DR, suggesting that autophagy is indeed important for survival in times of famine. Thus, initial findings suggest that autophagy restricts resources available for reproduction but is necessary for survival during famine, and are thus more consistent with the resource reallocation hypothesis.

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ELISA PEREZ BADAS

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Early-life conditions and their effect on senescence in European badgers: all's well that ends well?

Under the assumption that 'a good beginning makes a good ending' a wealth of studies in evolutionary ecology have explored the effects that the early-life environment may have throughout an individual's life. Traditionally, the silver-spoon effect hypothesis has predicted that harsh environmental conditions may constrain body development, leading to individuals born under good environmental conditions to outperform those born under adverse conditions.

Recent studies however, suggest that young individuals may adapt their physiology during early development in anticipation for their future environment. Indeed, the Predictive Adaptive Response hypothesis (PAR) predicts that fitness benefits should be highest when environmental conditions during early-life match conditions during adulthood. Studies on wild mammal populations that highly depend on climatic conditions provide valuable information to disentangle the effect of early-life ecological conditions on later-life fitness.

Using one of the longest running mammal populations worldwide and a set of climatic variables, I will explore how the environment experienced in early-life affects senescence in the European badger (Meles meles) as indicated by breeding frequency, offspring number and quality.

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HELENA WELLS

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A genome wide association study in the UK Biobank cohort identifies a large number of genome-wide significant loci linked to self-reported adult hearing ability

Background: Age-related hearing impairment (ARHI) is the most common sensory impairment in the aging population; over a third of individuals develop this complex trait by the age of 65. It is a multifactorial disorder with both genetic and environmental components, with estimates of heritability ranging between 35 to 55%. It is expected to be a highly heterogeneous trait given that over 150 genetic loci have been identified in non-syndromic hereditary hearing loss alone. Previous genetic studies into ARHI have successfully identified a number of promising candidate genes although only a very small number have reached genome-wide significance. However, replication of these findings across cohorts has been limited possibly due to varied phenotyping approaches and restricted sample sizes for genome wide analysis.

Methods: We performed two genome-wide association studies (GWAS) using self-reported hearing data from the UK Biobank (UKBB) study involving over 500,000 volunteers recruited between 40-69 years of age. Using a case control design we categorised participants based on answers to questionnaires regarding hearing ability (n=498,281) and hearing aid use (n=316,629). A linear mixed models approach was used to test for association between a total of 9,740,198 SNPs and the two hearing traits in white British participants. Final case control sample sizes for the association analysis were n=250,389 for self-reported hearing ability and n=253,918 for self-reported hearing aid use.

Results: A large number of SNPs were associated at genome-wide significant levels ($P < 5E-08$): 2,080 SNPs with hearing ability and 240 SNPs with hearing aid use. Conditional analysis with GCTA-COJO confirmed that these results represent at least 40 independent genome-wide significant loci. A number of these loci contain genes previously linked to congenital hearing loss such as EYA4, LMX1A and TRIOBP, however most loci appear to be novel associations with hearing.

Conclusion: Our study provides a new insight into genes which underlie susceptibility to adult hearing loss and thereby may be a first step towards a greater understanding of the pathological mechanisms involved.

MICRO TO MACRO

Chair: Frank Hailer

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MATTHEW T WEBSTER

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The genomic basis of local adaptation and speciation: lessons from birds and bees

As populations diverge and eventually form new species, several interacting processes lead to the accumulation of differences in their genomes. These include the formation of genomic incompatibilities, local adaptation, background selection, genetic hitchhiking, and gene flow. Disentangling the effects of these processes on genome variation is key to understanding how new species form. A genic view of speciation envisages the formation of genomic islands of differentiation in incipient species that are resistant to gene flow, which gradually expand in size until they generate complete reproductive isolation. However, evidence for the generality of this model is lacking.

Here I will present analyses of genome-wide comparisons between locally adapted populations of honeybees and between closely-related species of Darwin's finch. In both cases, locally differentiated regions of the genome contain haplotype blocks with reduced recombination rates that correspond to ancient balanced polymorphisms.

Similar observations have also been made in other taxa, suggesting that the presence of ancient balanced polymorphisms may be a common mechanism that facilitates local adaptation leading to speciation.

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Genetic differentiation among chimpanzee subspecies and adaptations to viral infections

How genetic adaptations contribute to the differentiation of diverging populations remains a fundamental question in evolutionary biology. Adaptation to disparate selective pressures can promote genetic and phenotypic differentiation, but dissimilar adaptations to common selective pressures, if common, could also contribute decisively to the differentiation of isolated populations. Here we explore this question in the four recognised subspecies of chimpanzee, which are our closest living relatives, and are endangered.

Collectively, the four chimpanzee subspecies inhabit the large area ranging from the centre to the west of central sub-Saharan Africa. Several selective factors differ among subspecies, and we used full genomes of dozens of individuals to investigate the differential adaptations among the four subspecies. A particularly interesting selective factor is the Simian Immunodeficiency Virus (SIV), which has been observed only in natural populations of two subspecies: the central and eastern chimpanzees. SIV is usually well tolerated by chimpanzees and does not result in immunodeficiency, even if central chimpanzees' SIV is the source of the human HIV epidemic. Our results show that adaptation to SIV can explain the major genomic signatures of positive selection in these two subspecies, suggesting that while not deadly, SIV remains a major selective pressure. Remarkably, adaptation differs between the two subspecies, with each of them evolving sets of genes with different roles in the infection. This shows how differing molecular mechanisms of adaptation to a shared pathogen have contributed to the genetic and phenotypic differentiation between these chimpanzee subspecies.

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Investigating genetics of hybrid dysfunction using inbred strains derived from natural populations in the house mouse hybrid zone

Hybrids between subspecies of house mice (*Mus musculus*) often show defects in fitness-related traits. We are investigating genetics of male sterility and gut microbiome composition in hybrid zone mice. Loci associated with these traits have been identified in natural populations, but the underlying genes are not yet known. Measuring fitness effects and characterising molecular mechanisms of a single locus in natural or outbred populations is challenging due to genetic variability among individuals.

To overcome this challenge, we have developed a panel of eight inbred strains derived from hybrid zone mice, which will enable characterisation of loci contributing to natural variation in quantitative traits, on identical genomic backgrounds.

We performed an intercross among the hybrid zone strains and mapped gut microbiome composition and testis defects with high resolution, including some loci containing a single gene. We discuss plans to profile individual strains to evaluate candidate genes and pinpoint the underlying molecular and developmental mechanisms.

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Understanding adaptive radiation and explosive diversification through cichlid fish genomics

Owing to their spectacular taxonomic, phenotypic, ecological and behavioral diversity and propensity for explosive speciation, the assemblages of cichlid fishes in the East African Great Lakes Victoria, Malawi and Tanganyika are prime role models in evolutionary biology. With the release of five reference cichlid genomes and many additional genomic resources as well as the establishment of functional genomic tools, the cichlid system has fully entered the genomic era.

The in-depth genomic exploration of the East African cichlid fauna — in combination with the examination of their ecology, morphology and behavior and information on the geological history of the Great Lakes — permits novel insights into the way how organisms diversify and how adaptive radiations progress.

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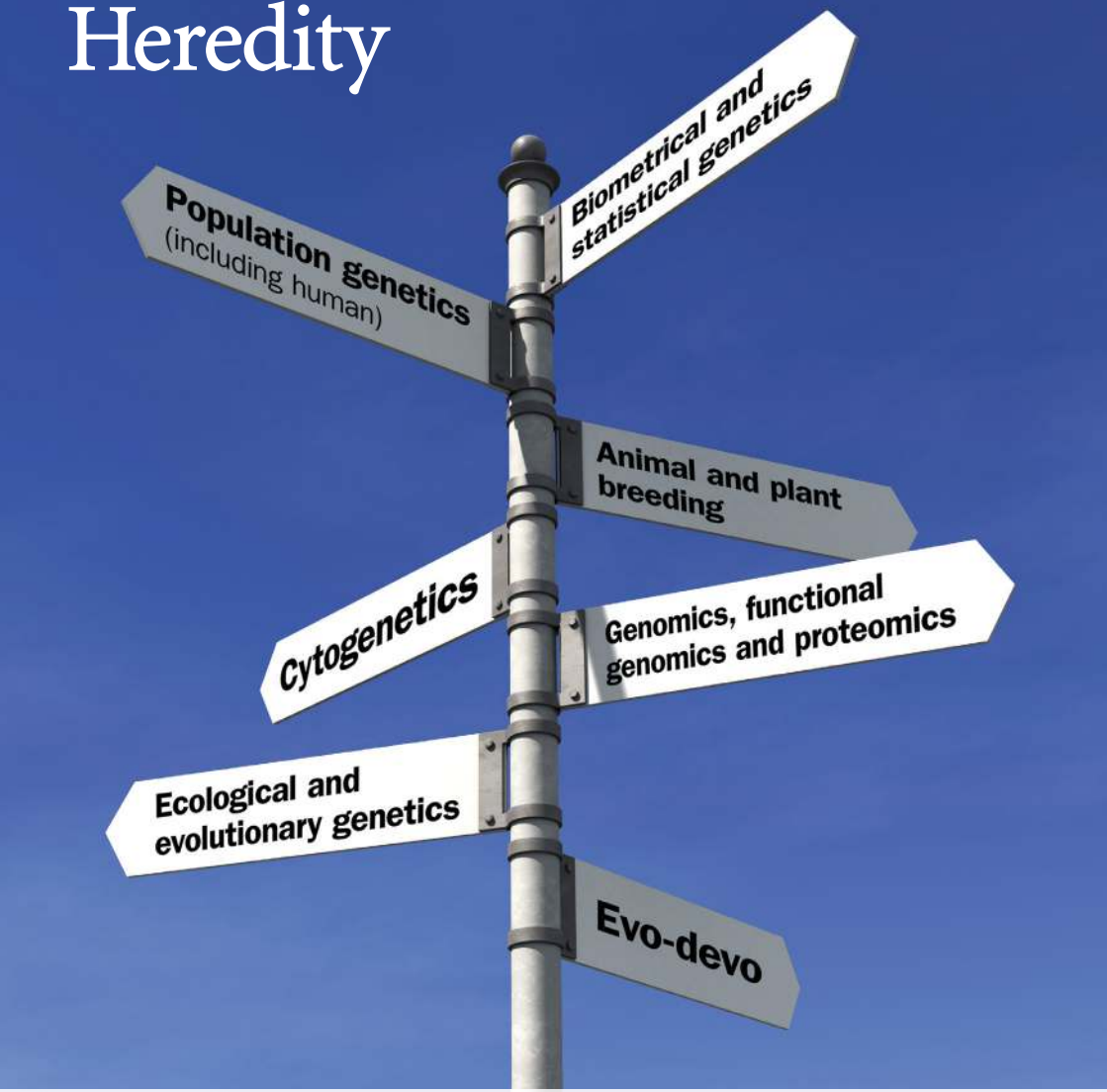

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POSTERS

Carbon for phosphorus trade in AM fungi in response to host adaptation

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The majority of land plants establish mutualistic symbioses with arbuscular mycorrhizal (AM) fungi. An association that benefits both partners by mediating uptake of essential plant nutrients, particularly P and N fueled by recently fixed carbon from host plants. AM fungi develop extraradical hyphal networks that link different plant species. The ability of the same fungal mycelium can colonize different plants at the same time involves an extraordinary level of compatibility and ability to adapt to different hosts by the fungus, though the adaptation to a single host might increase fitness of fungi at the expense of the other host. Our question is how plant and fungal fitness are linked and the genetics behind that. It has been suggested that AM fungi are heterokaryotic, contain genetically distinct haploid nuclei, and in response to a new plant species (changing environment), the developing fungal hyphae could temporarily segregate nucleotypes in the emerging spores to produce adapted offsprings that have different phenotypes than the parents. To test this, two green house, three-weeks-term experiments are being conducted to examine six plant species for their ability to host one of four fungal species in; one plant species system (one fungal and one plant species-study 1), and in a combination of two plant species system (one fungal and two plant species-study 2), in both studies spores were used as only inoculum. The best plant combinations that associate significantly with either fungus resulted from study (2) will be used in a study (3) to test the symbiotic performance of host-adapted fungus spores (generation 1) propagated in a two plant species system, when inoculated onto their same plant host species of (generation 2). In a three-semi partitioned microcosm, a nurse plant will be growing in the central compartment, and 50 spores of one fungal species will be applied to the soil. Upon mycorrhizal establishment, two-weeks-old test plants will be transplanted in the outer compartments, and the shoot of the nurse plant will be cut-off leaving the colonized roots in soil to enable the developing fungal hyphae to pass through a mesh barrier to the outer compartments to colonize the roots of newly applied plant. Symbiotic performance will be estimated using C to P trade in two generations. We will test for differences in C for P exchange between generations and if the one host-adapted generation will grow better at the expense of plant growth/fitness on the other host. The effect of the fungus will be assessed by comparison with control treatments in which fungus was not added. To investigate preferential plant C allocation and AM fungi P uptake, we will use radioactive isotope probing. 33P isotope application to the soil and 14C labeling. C to P ratio will be estimated using liquid scintillation counting. At harvest plant biomass will be assessed and fungal spore counts. The roots will be stained to estimate the colonization rate. If we observe fungal fitness changes in response to host adaptation, genomic basis for this pattern will be analyzed using single cell genomics technique.

Genetics, Epigenetics and Temperature Sensing in a Natural Environment

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Plants use environmental signals such as temperature to align their development with the seasons, and so maximise their reproductive success. The molecular mechanisms downstream of temperature sensing are known to be complex and, in some cases, involve epigenetic memory of the temperature signal. In Arabidopsis, the control of flowering time comprises the cold-induced epigenetic silencing of FLOWERING LOCUS C (FLC). Using experiments in natural field conditions, combined with mathematical modelling, we found that temperature sensing occurs at almost every step in the regulation and silencing of FLC expression. What is more, we found that diverse features of the fluctuating temperature signal are captured by different steps. Intermittent cold temperatures in early autumn were enough to promote transcriptional shut-down at FLC, but the epigenetic pathway was not activated. Only after temperatures stopped fluctuating to above 15°C, did we observe the upregulation of VERNALIZATION INSENSITIVE3 (VIN3), a key component of the epigenetic silencing. Thus, it is lack of spikes to high temperature, rather than just prolonged cold, which is the major driver for epigenetic memory. The mathematical model we developed was crucial to uncovering the temperature sensing properties of this system. Further, it has allowed us to identify mechanistic differences between Arabidopsis accessions that we can relate to known genetic variation. Finally, we can now exploit it to predict vernalization, a key process in determining plant fitness, in warming climates.

Why So Sterile? Investigating Hybrid Sterility in the House Mouse

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Mechanisms of the early stages of speciation can be understood by identifying barriers to gene flow between naturally hybridising species. A common barrier between recently diverged species is reduced fertility in hybrids. The house mouse subspecies, Mus musculus musculus and Mus musculus domesticus, meet and interbreed in a natural hybrid zone running through central Europe, and hybrid male sterility has been observed as a barrier to gene flow in these house mice. Here we use crosses of wild-derived M. m musculus and M. m. domesticus strains to investigate reproductive phenotypes to determine the number, type, severity and prevalence of fertility defects present. Complete sterility appears to be absent in the hybrid crosses, but a large proportion of males exhibit phenotypes below the range in pure subspecies, and likely suffer reduced fertility. The comparison of phenotypes indicates reduced hybrid fertility is highly variable among individuals, suggesting multiple underlying genetic incompatibilities are responsible for segregation in the hybrid zone. These results will be used in quantitative trait locus (QTL) mapping to identify loci contributing to sterility phenotypes.

Oral-facial digital syndrome associated with a recurrent homozygous splice site variant in TBC1D32

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The oral-facial-digital syndromes (OFDS) are a clinically and genetically heterogeneous group of conditions. They are characterised by facial, oral and digital anomalies associated with a wide range of additional features used to delineate subtypes. Currently 16 subtypes are listed on OMIM. However, there is considerable overlap between these and, in children diagnosed with OFDS, the exact classification can be difficult to determine. At least 17 cilial genes have previously been implicated in OFDS, some in association with more than one subtype, or another ciliopathy such as Joubert syndrome or Meckel-Gruber syndrome.

We report a family in which the proband presented with features suggestive of OFDS, including midline tongue groove, a high, narrow palate, ankyloglossia, choanal atresia and post-axial polydactyly. She had MRI brain scan anomalies, including septo-optic dysplasia (small anterior pituitary and optic chiasm with absent posterior pituitary) and cerebellar vermis dysplasia with Molar tooth sign, but no retinal problems. Her growth was suboptimal with a GH concentration of 0.6 ug/L in response to hypoglycaemia and undetectable/low IGF1 and IGFBP3. She was commenced on GH treatment with a good response. In a subsequent pregnancy, terminated due to likely recurrence, the fetus had a midline cleft lip and partial intestinal malrotation. The clinical picture in this family was felt to be consistent with the subtype OFDVI on the basis of the MRI brain scan findings.

Whole genome sequencing was carried out via the 100,000 Genomes Project. Both the affected proband and fetus were found to have a homozygous splice site variant in TBC1D32, a gene known to play a role in ciliary morphology. This variant (c.1372+1G>A) has been shown to abolish the consensus donor site downstream of exon 12, resulting in in-frameshift truncation of 47 amino acids (p.Arg411_Gly458del). The same variant has previously been reported as a variant of unknown significance in a single case, with similar clinical phenotype, classified as OFDIX due to the presence of retinal anomalies.

This family confirms the association between TBC1D32 and OFDS and provides further information about the clinical findings related to this genotype. This finding also highlights the difficulty in assigning an individual gene (and a previously described variant) to a specific, rare OFDS subtype. We support the recent suggestion that clinical classification of OFDS is restricted to the three most common/well-delineated subtypes (OFDI, OFDIV and OFDVI), with further classification based on genotype.

Oral-Facial-Digital Syndrome Due To a Mutation In TBC1D32: A Further Case Report

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In this report, we describe a girl with oral, facial and digital anomalies including abnormalities of the palate, strabismus and postaxial hand polydactyly. She also presented with several CNS anomalies, hearing and visual impairment, and global developmental delay. Whole genome sequencing of the patient revealed a homozygous splice site mutation in TBC1D32/C6orf170 (c.1372+1G>A). The same mutation has been previously reported as a single case in 2014 and was concluded to best fit OFD type IX. c.1372+1G>A is currently classified as a variant of unknown significance because its contribution to OFD type IX has not yet been confirmed. This paper confirms the pathogenicity of this mutation and concludes that, based on the findings, the phenotype is in fact more consistent with OFD type VI.

Skates on thin ice: a phylogenetic study of vulnerable elasmobranchs.

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Batoid fishes (skates and rays) are among the most endangered marine vertebrates, with around 20% now threatened with extinction. Typical of predatory organisms, they can be characterised by a large size, slow growth rates, late maturity, and low fecundity, making them intrinsically at high risk of overexploitation by fisheries. Despite this, the high levels of morphological and ecological conservatism among extant orders has resulted in a great deal of taxonomic confusion and unstable nomenclature, confounding conservation efforts. Recent advancements in molecular genetics have even enabled the detection of cryptic species (species that look alike but are genetically distinct) and species complexes within the Batoidea. Although this issue is receiving more scientific attention, taxonomic questions still surround many species, some of which this Masters project aims to resolve. Namely, are the thornback ray (*Raja clavata*) and Madeiran skate (*Raja maderensis*) distinct species; are the Norwegian skate (*Dipturus nidarosiensis*) in the Mediterranean distinct from those across the rest of the North Atlantic; is there a new species of endangered cryptic skate in the Azores? Mitochondrial DNA (mtDNA) and restriction-site associated DNA sequencing (nextRAD-seq) are being utilised, with strong conservation implications for these threatened species of fish.

Genetic basis and timing of a dominant loss of self-incompatibility in *Capsella orientalis*.

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Plants evolved complex strategies to promote cross-fertilisation, yet shifts from outcrossing to self-fertilisation are frequent and often involve the breakdown of genetic outcrossing mechanisms. In Brassicaceae, self-incompatibility (SI) allows plants ensure outcrossing by rejection of self-pollen on the stigma. This occurs through the interaction of female and male specificity components, which consist of a pistil based receptor and a pollen-coat protein, both of which are encoded by tightly linked genes at the S-locus. When benefits of selfing are higher than costs of inbreeding, loss-of-function mutations in the male (pollen) SI component should be favoured, but the role of parallel molecular changes for convergent phenotypic evolution remains unclear. The crucifer genus Capsella offers an excellent opportunity to study multiple transitions from outcrossing to self-fertilization, but so far, little is known about the genetic basis and timing of loss of SI in the self-fertilizing diploid *Capsella orientalis*. Here, we show that loss of SI in *C. orientalis* occurred recently (<2.5 Mya) and maps as a dominant trait to the S-locus. Using targeted long-read sequencing of multiple complete S-haplotypes, we identify a frameshift deletion in the male specificity gene SCR, and we confirm loss of male specificity in *C. orientalis*. We further analyze RNA sequencing data to identify a conserved, S-linked small RNA (sRNA) that could explain dominance of self-compatibility. Our results suggest that degeneration of male SI specificity in dominant S-alleles is important for shifts to self-fertilization in the Brassicaceae.

The Development and Genetics of Carnivorous Traps

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Leaves display amazing diversity and complexity in size, shape and adaptation. Many leaves are flat, planar outgrowths where shape is determined by margin and thickness. One of the most complex leaf structures found in nature are the three-dimensional cup-shaped (epiascidiate) leaves of certain carnivorous plants. Considering it is such a complex shape, it is surprising that epiascidiate leaves have evolved independently in four different families: Nepenthaceae, Sarraceniaceae, Cephalotaceae and Lentibulariaceae. A key question is, are the genetic and mechanistic rules underlying leaf development conserved between two-dimensional and three-dimensional leaves? To elucidate how an epiascidiate leaf shape forms I study the carnivorous traps of the humped-bladderwort (*Utricularia gibba*). *U. gibba* is particularly amenable to study due to its small size, ease of growing in glasshouse and tissue culture and transparent traps, which are only two cell layers thick. It

also has one of the smallest genomes know in the plant kingdom (~100Mb), which makes it amenable to genetic studies and whole-genome sequencing.

Here, I present the work on a forward genetic screen on a population of *U. gibba* where mutants with a bladder shape phenotype have been found and how candidate mutations have been found, along with descriptive phenotyping of mutant traps to compare and contrast with wild-type traps. Future steps to identify causality and cellular phenotypic characterisation are given that will help answer: how do traps develop their shape?

Genetic variation on resistance in *Drosophila melanogaster* against *Drosophila* C virus

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Why some individuals are less resistance to parasites than others? Some evolutionary models predict a continuous evolving gradient of resistance/susceptibility between host and pathogen across population which may lead to a differential level of resistance. This would imply that some host genotypes in population should be more resistance to certain pathogen genotypes than others. This project uses *Drosophila melanogaster* as model system for studying the genetic association of host and pathogen genotypes. Drosophila populations are actively exposed to a specialized RNA virus pathogen, *Drosophila* C virus (DCV). In response, Drosophila populations have a group of allelic variants on a single gene called pastrel which confers differential levels of resistance to DCV. Here, I study whether there is specific interaction between the polymorphic variants of pastrel in *Drosophila* and different DCV genotypes. There was no interaction between *Drosophila* and DCV genotype, but the *Drosophila* genotype explained most of the genetic variance in resistance to DCV. Some flies carrying the pastrel variant for susceptibility were more resistance to DCV than some flies carrying the variant for resistance, indicating that other genes can contribute to the protection. In summary, this research reflects a complex co-evolutionary dynamic between a specialized RNA virus pathogen and *Drosophila*, where the pathogen genotypes are controlled by a group of polymorphic variants ancestrally maintained in the populations of *Drosophila melanogaster*.

The invasion of *Perophora japonica* in Plymouth

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Invasive species, which are not native to a region and have often been introduced by our actions, can be extremely harmful. Once introduced they can be freed from competitors and disease (so called 'competitive release'), damaging ecosystem function and threatening native species/biodiversity. The introduction of invasive marine species has been identified as a major threat to the world's oceans, where they can spread to new environments via ships through ballast water or hull fouling. In particular, sedentary species that attach to submerged structures like boats, marinas & rigs cause damage and are associated with huge economic costs to remove them.

This project focuses on a non-native sea squirt (*Perophora japonica*) that has colonised marinas across Europe. It will extend a unique timeline of molecular data (specifically COI sequencing) to investigate how genetic diversity has changed in populations since the introduction (Pérez-Portela et al., 2012). This is a key question in population genetics as the relationship between genetic diversity and introduction success has not been clearly established - how do small numbers of invading organisms with very low genetic diversity even survive in completely new environments? The exceptional element of this project is that samples have been collected in one marina at a geographically fine-scale for almost 20yrs, allowing detailed examination of the temporal changes in genetic diversity and bottlenecking since the first invasion. I am particularly interested to talk about evidence (or lack of) for subsequent invasions that may have 'rescued' genetic diversity with the introduction of new individuals. These are fundamental questions in ecological & population genetics theory, but also relate to the applied threats of invasive species and their associated economic cost.

I have spent several months at the University of Exeter analysing *P. japonica* gathered from Queens Anne's Battery Marina (Plymouth) as part of an internship and will continue to study it as my 3rd year dissertation project starting September 2018. Previous work has analysed the population since its invasion, up to 2007 – and I am extending this timeline to the present day. Also, if there is sufficient time, I will develop and test primers targeting nuclear DNA, which could provide additional insights into the genetics of this invasion.

Mito-nuclear genotypes modulate metabolism with downstream fitness consequences

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Mitochondria are essential for eukaryote evolution, taking centre-stage in the process of cellular respiration. This process is regulated via a series of finely coordinated interactions encoded by two obligate genomes – nuclear and mitochondrial. Both genomes are required for the production of cellular energy, and thus their harmonious interaction is essential to maintain mitochondrial integrity and the viability of eukaryote life. Although these interactions are highly important for organismal fitness, we do not know the mechanisms that underpin these processes. Here we aim to unravel these complex inter-genomic interactions by examining the physiological and fitness consequences of mito-nuclear incompatibilities using Drosophila melanogaster. We additionally examine how mito-nuclear interactions impact fitness across different levels of cellular stress (induced by antioxidants). We find that antioxidant stress has a significant effect on all strains, however the magnitude of the response was heavily dependent on the mito-nuclear combination of the given fly strain. We then hone in the physiological responses underpinning the observed fitness outcomes, and find that metabolic processes also greatly depend on the mito-nuclear genotype. By examining physiological traits, we create more direct link between genotype, metabolic phenotype and fitness. These findings highlight the need to examine intermediate phenotypes in order to fully comprehend fitness consequences of diverse genotypes.

Dissecting the genotype-phenotype-fitness map for traits mediating sexual attractiveness

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Understanding the maintenance of genetic variation requires dissection of the relationships between genotype, trait, and fitness. In this talk, I highlight how both genomic and classic quantitative genetic approaches can be integrated to achieve this goal. The sexual communication system of the fly, *Drosophila serrata*, comprises multiple contact pheromones (cuticular hydrocarbons, CHCs). In males, these traits are under strong sexual selection through female mate choice. To date, little is known of the polymorphisms underlying these important traits nor, critically, the population frequencies of causal alleles. To examine the genetic basis of sexual attractiveness in this system we took an integrated approach. A replicated PoolSeq GWAS on two composite traits; the combination of CHCs under very strong sexual selection and a combination of CHCs under weak sexual selection revealed striking differences in genetic architecture. Results point to a complex basis to sexually-selected CHCs but surprisingly, CHCs under weak selection are dominated by a major gene. A ten-generation artificial selection experiment on the sexually selected CHCs revealed abundant heritable variation to increase trait values and that the increase boosted male attractiveness. However, when selection was relaxed for five generations, traits regressed towards their starting values indicating fitness trade-offs. It appears therefore that while standing variation is shaped by direct sexual selection in these traits it is also affected by selection operating on other traits that have pleiotropic relationships to male CHCs. These results highlight the importance of considering how pleiotropy affects the genotype-phenotype-fitness map.

Signatures of selection revealed by population analyses of bumblebee genomes.

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Insect pollinators, including social bees, are key to ecosystem stability, as well as agricultural yields. Recent bee declines are suggested to be caused by a number of contributing factors, such as land-use change, pesticide exposure, climate change, pathogens and newly emerging diseases. However, our understanding of the potential effects of such stressors on wild pollinator species at the molecular and genomic level is limited. To help understand the relative impacts of these competing challenges, we conducted a population genomic study on the buff-tailed bumblebee, Bombus terrestris, a common Eurasian species and important ecological pollinator. From 28 sites across the island of Britain, we sampled wild individuals and performed whole-genome sequencing. We identify the presence of recent selective sweeps affecting genes involved in important

biological processes, such as immunity, neurology, as well as detoxification processes. Furthermore, we identify conserved gene-rich regions under selection within other social bees. Taken collectively, the results provide an insight into ongoing selection and recent evolutionary history of this important ecological insect pollinator.

Population epigenetics in *Timema cristinae* stick-insect

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Epigenetic factors can contribute to phenotypic diversity. For instance, DNA methylation can influence gene regulation, and thus phenotypic plasticity. However, little is yet known about how and why methylation varies in wild populations. Here, we described and investigated whole-genome methylation profiles in populations of the stick-insect *Timema cristinae*, depicting the factors shaping the methylation patterns. We tested the hypotheses that natural methylation variation is structured in geographical space and correlated with environmental factors such as host-plant and climate. We further tested for genetic variation in methylation status. Using data obtained from whole-genome bisulfite sequencing, we found that methylation variation in CpG context tends to cluster following the geographical distribution of populations. Using binomial mixed models, we not only found association between methylation levels and environment, but also evidence for genetic variation and moderate heritability in methylation status, suggesting variation can be accumulated in populations.

Allele Age Under Non-Classical Assumptions using an Exact Markov Chain Approach

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Determination of the age of an allele based on its population frequency is a well-studied problem in population genetics, for which a variety of approximations have been proposed. We present a new result that, surprisingly, allows the expectation and variance of allele age to be computed exactly (within machine precision) for any finite absorbing Markov chain model in a matter of seconds. This approach makes none of the classical assumptions (e.g., weak selection, reversibility, infinite sites), exploits modern sparse linear algebra techniques, integrates over all sample paths, and is rapidly computable for Wright-Fisher populations up to an effective population size of 100,000. With this approach, we study the joint effect of recurrent mutation, dominance, and selection. These results highlight the under-appreciated utility of computational methods for the direct analysis of Markov chain models in population genetics.

Fitness consequences of germline mutation load: the hidden cost of lifespan extension?

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Central to the evolutionary theory of ageing is the assumption that trade-offs between longevity and reproduction are ubiquitous. Yet it is becoming increasingly apparent, across a number of empirical studies, that lifespan extension is not always dependent on a cost to fecundity. We propose that this apparent cost-free lifespan extension, can be explained by the hidden costs of reduced germline maintenance, leading to a trade-off between parental longevity and offspring fitness.

The most compelling example of cost-free lifespan extension is the downregulation of nutrient-sensing signalling in *C. elegans* nematodes, using daf-2 RNAi knockdown in adult worms, making them extremely long-lived and stress-resistant with normal reproduction. We use mutation accumulation (MA) approach to directly compare mutation rate and fitness decline in replicate daf-2 RNAi and sham control MA lines following UV-induced germline mutations. We predict that increased investment into somatic maintenance via interference with nutrient-sensing molecular signalling will result in increased mutation rate and reduced offspring quality. The work ultimately contributes to determining the evolutionary and genetic constraints on the evolution of longevity.

Genetic Diagnosis of Heterogeneous Conditions Applying Targeted Gene Capture and Next-generation Sequencing

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The genetic heterogeneity of certain conditions poses a medical challenge as different types of the same disease often display varying severity, prognosis, treatment and inheritance. Differential diagnosis methods have traditionally been used to elucidate the form of these diseases. However, the efficiency of said differential procedures is limited at diagnosing rare or de novo variants.

We aimed (1) to overcome the diagnostic limitations of differential procedures and (2) to detect the genetic and protein sequence variants present on each patient to enable precision medicine. Applying selective genomic enrichment in combination with next-generation sequencing (NGS), we performed a targeted gene capture of the genomic regions accounting for different subtypes of heterogeneous diseases. We present a novel diagnosis methodology that was validated by successfully diagnosing 29 patients with diverse types of cardiopathy, Charcot-Marie-Tooth (CMT) disease and Maturity Onset Diabetes of the Young (MODY).

The landscape of coadaptation in *Vibrio parahaemolyticus*

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We exploit the nearly panmictic population structure of the gastric pathogen Vibrio parahaemolyticus to perform a genome-wide screen for coadapted genetic elements. The great majority of interactions that we detect are between accessory genes, many involved in carbohydrate transport and metabolism. The most complex co-adaptations we identify include hundreds of core genome SNPs and accessory genome elements and involve genes encoding lateral flagella and cell wall biogenesis, implying that several strategies have evolved for colonizing surfaces. Our results provide evidence that, as in human relationships, coadaptation involves progressively increasing levels of commitment, with the most involved interactions becoming irreversible and presaging speciation.

Characterisation of the RDL A301S mutation in *Plutella* xylostella using CRISPR/Cas9

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Mutations in the GABA-gated chloride channel are associated with resistance to cyclodiene organochlorine and phenyl pyrazole insecticides. The best characterised of these is A301S, which was initially identified in a Dieldrin resistant strain of *Drosophila melanogaster*. The orthologous mutation has been found in a variety of different crop pests including the diamond back moth *Plutella xylostella*. There is however some ambiguity over the extent of its contribution to resistance in this species. We have used the CRISPR/Cas9 system in order to edit *Plutella* PxGABARalpha1 to serine at the 301 orthologous position (282 in PxGABARalpha1) in an insecticide sensitive isolated. By uncoupling RDL 301S from other resistance mechanisms that are potentially present in resistant field isolates, we can determine its contribution to cyclodiene organochlorine and phenyl pyrazole resistance. This type of approach improves our understanding of resistance and the interaction of insecticides at their targets, enhancing our design led capabilities for novel insecticides. Using CRISPR/Cas9 we can better tailor insecticide design for specific pest species.

Sequencing-era methods for identifying signatures of selection in the genome

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This presentation is a review of recently published methods for identifying signatures of selection in the genome. The rationale for the methods is discussed, as well as the pitfalls and other confounding factors. Four of the methods are applied to simulated datasets for comparison.

Understanding the underlying genetic cause of the phenotypic variation we see around us is vital in the study of adaptation and evolution. The current availability of whole genome sequence data and the rise of computing power means we have the opportunity to discover more than ever before. This has necessarily led to the development of methods to interrogate the data for evidence of natural selection.

The methods which have been developed and published in the last few years range from simple statistics through to complex machine learning approaches. Fourteen recent methods have been reviewed: nine statistics based on linkage disequilibrium, haplotype homozygosity, composite likelihood and time to most recent common ancestor; two statistics that are a composite of other statistics; and three machine learning methods.

As a proof of concept, four of these methods were applied to simulated datasets. Two populations were simulated using the software "msms": a neutral population and a population undergoing positive selection. ROC curve analysis was performed, with two of the methods - Z and H12 - achieving an area under the curve of 100% for these simulations. The rationale behind the methods has been explored, showing how selection for an allele can leave behind signatures in the genome as other nearby variants "hitchhike" along with the selected variant, creating highly correlated alleles in regions of the chromosome. Also discussed are the pitfalls and other confounding factors which affect the methods and can lead to false positives, such as demographic changes, recombination and irreproducibility of results.

Fruitless as a candidate sexual antagonistic gene in *Drosophila melangaster*

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The sexes are shaped by selection to play different reproductive roles, resulting in dimorphism in behaviour, physiology, and morphology. However, since the sexes share most of their genetic material, selection for dimorphism can cause adaptive conflict between the sexes, where genetic variants are beneficial in one sex but detrimental in the other - sexual antagonism (SA). Quantitative genetics studies have shown that sexually antagonistic genetic variation is common across species. However, there has been some difficulty in identifying the genes underlying antagonism. Here, we take a candidate approach and focus on the gene fruitless in *Drosophila melanogaster*. This gene plays an important role in sexual development yet its sequence shows significant and stable genetic polymorphism within populations of D. melanogaster. We assess potential antagonistic selection on fruitless variants in two ways. Firstly, we directly measure male and female fitness in lines carrying alternative fruitless alleles in an otherwise identical genetic background. Second, we assess the presence of antagonism-mediated balancing selection by tracking the frequencies of alternative fruitless alleles in cage populations that have been set up at different starting frequencies (1:9, 9:1). We find that allele frequencies converge in cage experiments, compatible with the presence of balancing selection on fruitless. Direct measures of fitness show that while lines vary in sex-specific performance, they do not show consistent differences in fitness effects between lines carrying alternative alleles, possibly due to confounding effects of linked genetic variation within individual lines. While further work remains to be done, our experiments suggest that antagonistic genetic variation can affect even key regulators of sex-specific development.

Evolution on Ice: Omic insights into Molecular Adaptation in Antarctic Sponges

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Animals in the Antarctic seas have adapted to some of the most challenging conditions found anywhere on Earth. Temperatures ranging between 0 and -1.8°C and a food supply which fluctuates widely render their survival difficult. Nevertheless, species have found the means to thrive in such conditions. Sponges are particularly important members of Antarctic ecosystems, but to date our knowledge of how they endure these temperatures is limited at best, especially at a molecular level.

We aim to identify the mechanisms by which sponges have adapted to such extreme environments by contrasting congeneric species pairs adapted to vastly differing thermal conditions. These aims are being accomplished using transcriptomic and genomic sequences from the genera *Axinella, Mycale* and *Phorbas*. These are abundant in the Antarctic, Caribbean and Mediterranean, and play essential roles in the benthic ecosystems in which they are found. Particularly, we have sequenced multiple transcriptomes from 10 target species, as well as the genomes of *Mycale acerata* and *Mycale laevis*, and are supplementing our "omic" work with targeted in situ and functional experiments.

Using this data, we have performed a number of tests for selection (particularly in Hyphy/CODEML) and identified genes with multiple lines of evidence for positive selection. 10 genes with perfectly congruent results from all tests are of particular interest, including eukaryotic initiation factors and SPRY domain containing proteins, as well as a number of phylogenetically well-conserved "housekeeping" genes. We have also analyzed differential gene expression and content. With this data, we can state which genes are vital in cold conditions, and when adaptive molecular mechanisms have been used broadly, convergently, or in vastly varying ways across sponge and animal phylogeny.

Designing phenotypes through genome editing: from current examples to future perspectives

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Selection based on beneficial traits such as yield, pest/disease resistance or end-use qualities has been the basis of crop improvement for thousands of years. Nowadays, we have a better understanding of the genetics that underpin specific crop traits, which can be applied to enhance breeding. Random mutagenesis resulting from radiation or chemical treatments can generate valuable genetic variation for breeding, but the level of undesired changes in the plant genome and the significant challenges, resulting, for example, from linkage drag, to isolate beneficial mutations from the non-desired ones have led to the

search of alternative tools. Transgenic crops, despite the controversy behind their safety and further commercialization, are a different option for generating novel traits. However, the legislative hurdles around their use and commercialization make them unavailable for their common use in breeding. In the same group of techniques, genome editing has been a promising technique to mimic natural mutations with a high level of target specificity and simplicity in design and use.

The use of these type of techniques has relied on the use of model plants to extrapolate the results to crops with commercial interest. In that regard, we will discuss different examples of edited crops with enhanced commercial traits and how these relate to work done in different species. We will illustrate this with work we are doing to develop high throughput gRNA screens in protoplasts of *Brachypodium distachyon*, a model plant from the Poaceae family, which has not been reported to be editable using CRISPR/Cas, unlike other members of the family like barley, wheat and rice.

The evolutionary genetics of multidimensional plasticity in a wild seabird

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Phenotypic plasticity is defined as the ability of a single genotype to alter its phenotype in response to environmental variability. A vast body of empirical work shows that plasticity is widespread and ubiquitous across natural populations, and that it is an important means by which organisms adapt to spatio-temporal environmental heterogeneity. Furthermore, if individual variation in plasticity exists and has a heritable component, plasticity is predicted to evolve when selection favours more or less plastic individuals. Traditionally, studies on plasticity have mostly focused on single environmental factors and one-dimensional response variables. However, empirical investigation of the evolutionary genetics and patterns of selection of multi-trait and multi-driver plasticity would allow us to extend and generalize our knowledge in this field. I will present a project where we aim to integrate the study of multiple intrinsic and extrinsic drivers of plastic responses in multiple trait types at multiple levels of variation. To do so, we investigate the evolutionary genetics of plasticity in a natural population of a relatively long-lived seabird under long-term investigation, the common tern *Sterna hirundo*.

Colourful males and the maintenance of adaptive polymorphism in the Trinidadian guppy, *Poecilia reticulata*: a balancing act

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A classic understanding of evolution is that a genetic trait which increases the fitness of a population will sweep to fixation, thereby eroding diversity at this site. However, this simple model does not account for the high amount of diversity that is often observed in ecologically important traits. Balancing selection is an umbrella term for the evolutionary processes that maintain such diversity. But which genes are the target of balancing selection? And do they vary across populations? Using a variety of genomic analyses, we are interrogating the ecological genomics of Negative Frequency Dependent Selection (NFDS) in the Trinidadian guppy (*Poecillia reticulata*). Guppy males are colourful, displaying a mosaic of complex and varied colouration patterns; in comparison, females are drab and inconspicuous. Experimental manipulations of natural populations show that females prefer rare males and that rare males show higher reproductive fitness. Moreover, rare males have a significantly higher survival advantage, presumably due to reduced predation. Examining data from 13 natural populations sampled across a range of colour and predation schemes, we are using genome scans to identify the evolutionary signatures of balancing selection. We will investigate whether the targets of balancing selection vary across different populations, in relation to the predicted ecological differences in natural (predation) and sexual (female preference) selection pressures. By combining estimates of ecological selective pressures and the genomic signatures of that selection across populations, we will be able to better understand the process of balancing selection and the interplay between natural and sexual selection.

Factors impacting in silico identification of the bear Y-chromosome

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Haploid sex chromosomes such as the mammalian Y and the avian W are rich sources of evolutionary information, but have remained largely unexplored in most taxa. Recent work has identified sex-linked scaffolds from genomic assemblies based on the predicted differences in sequencing coverage between males and females (e.g. average depth (AD) ratio), but the factors governing non sex-dependent sources of variation in sequencing coverage are not well understood.

We here evaluate AD ratio results from whole-genome sequences of 5 male and 5 female brown bears, a model organism in conservation genetics and phylogeography. Twenty-five genomic scaffolds covering 1.74 Mb of the heterogametic reference assembly

were consistently categorised as Y-chromosomal across genomic comparisons, and also congruent with results from a previous study on other bear genomes. These 25 scaffolds should be prioritised for use in male-specific marker development in future studies. Variation in average sequence coverage across a scaffold was found to be the most important variable predicting variation in AD ratio results, and precision of sequencing coverage estimation appeared lower for shorter scaffolds, with unreliable results obtained for scaffolds <3 kb. Our work demonstrates that the AD ratio approach can reliably identify sex-linked scaffolds, and we outline strategies that are likely to yield more robust results. These results indicate that sex chromosome sequences will likely see increased use in evolutionary studies in coming years.

How predictable are you under pressure? Among-individual variation in behavioural predictability.

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Exploring the causes and consequences of consistent among-individual differences in mean behavioural traits ('personality') has been the focus of a large body of research within the fields of behavioural ecology and evolutionary biology. Many statistical approaches used to quantify consistent differences in individual behaviour assume within-individual variation is homogenous across individuals. However, within-individual variation has recently been observed to consistently differ across individuals, i.e. some individuals consistently behave more predictably across time and context than others, in part as a consequence of genetic variation. This among-individual variance in behavioural predictability' may have broad biological implications to the study of behaviour. As an example, behavioural traits play an important role in the stress response. The dominant model of variation in the behavioural stress response posits that individuals, and genotypes, will vary along a proactive-reactive axis, where proactive individuals consistently engage in bold behaviours when encountering novel, risky and stressful situations. Recently, it has been suggested that within-individual variation in these responses may also exist, where proactive individuals display consistently more predictable or stereotyped behaviour than reactive individuals. Although among-individual differences in behavioural predictability have been suggested, standardized studies on how best to quantify it are limited. Here, we conduct a repeated measures experimental design to test for among-individual differences in mean behaviour and predictability in risk taking behaviours in the Trinidadian guppy (*Poecilia reticulata*). We used a double hierarchical generalized linear model (DHGLM) method to simultaneously estimate among-individual variation in mean behaviour and predictability. This model is an extension of the linear mixed model that exploits the fact that variation in variances, as well as variation in means, can be

modelled simultaneously within the same framework. We found significant repeatability in all stress related behavioural traits assayed, consistent with the presence of among-individual variation in behaviour within the population. By applying DGHLMs we also show that guppies vary in behavioural predictability. Furthermore, extending out analysis to further utilise available pedigree data, we are able to show that heritable effects underpin individual difference in (average) behaviour and predictability. These findings show that within-individual variation is not homogenous across individuals or genotypes, a result that may mean some caution is required when interpreting statistical analyses assuming homogeneity of residuals, but which also sets the stage for development of hypotheses about the causes and consequences of variation in behavioural predictability.

High-throughput screening of fluorescent RNAs mutants in various conditions.

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The discovery of Green Fluorescent Protein few decades ago has revolutionized the way we do molecular biology research. Today we are witnessing a similar process in the RNA world with the development and utilization of various RNA mimics of the GFP such as Spinach and Broccoli, which bind different chemical fluorophores with high affinity and induce their fluorescence. They can be fused to RNAs expressed in the cell and used for investigation of their localisation and stability in vivo. Here we show how we repurposed commercially available gene expression microarray for high-throughput screening of fluorescent RNAs. We designed a library of all possible single and double mutants of the Broccoli RNA aptamer and all single and all single and a fraction of double mutants of Spinach RNA, with each variant repeated 4 times and fused to a different sequence complementary to a specific probe on the microarray. We used microscope imagining to measure fluorescence of each mutant from library in various conditions, like different concentrations of magnesium, potassium or fluorophore. Among other possibilities such approach will potentially provide a set of well characterised aptamers which can serve as fluorescent intracellular sensors of ions concentration.

Using CRISPR-Cas9 to target antimicrobial resistance genes in human gut microbial communities

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CRISPR-Cas systems have the potential to be developed as a new tool to combat healthcare-associated antimicrobial resistance in human gut bacteria. However, delivery of a system able to cure bacteria of drug-resistance plasmids or kill resistant organisms will be challenging in a spatially complex and biologically diverse bacterial community. We are attempting to use broad host range conjugative plasmids as a delivery vehicle to target drug-resistant clinical isolates, such as Enterobacteriaceae and Enterococci, in these environments. The efficiency of plasmid spread and its ecological consequences in these communities will subsequently be assessed, as well as strategies to combat the evolution of resistance to CRISPR-Cas9.

Genetic constraints on adaptive phenological traits in poplar

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The transition between growth and dormancy represents an important trade-off between growth and damage minimisation of perennial plants. Here we investigate how genetic covariance between phenology traits and growth may constrain adaptive evolution. We analyse phenology measurements drawn from 546 established trees in a growth trial in central Sweden, and use a quantitative genetic animal model to estimate trait heritability, genetic (co)variances and correlations between phenology traits and growth. We find moderate heritabilities (0.43-0.58) for all phenology traits and for lifetime growth (0.54). There was no genetic association between bud break and growth, possibly due to the unpredictability of spring temperature which is an important cue for this developmental transition. Leaf unfurling was negatively correlated with lifetime growth, reflecting reduced growth in trees with delayed leaf unfurling. Autumn phenology has strong genetic correlations with growth where late leaf senescence extends the growing season resulting in higher growth. These genetic relationships reflect an adaptive significance to growth phenology, with the strongest genetic covariances between phenology and growth in autumn traits.

Genetic architecture of behavioural syndromes in field crickets: adaptation or constraint?

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Genetic correlations have the potential to impose constraints on the evolution of populations. These potential constraints have been shown to be greater for behavioural traits versus either life-history or physiological traits. However, the long-term evolutionary consequences of behavioural syndromes depend on whether such correlations originate from pleiotropy or selection-induced linkage disequilibrium. Correlations due to pleiotropy are expected to be more stable and impose longer-lasting constraints on evolutionary trajectories than those originating from drift or linkage disequilibrium. Using field crickets (*Gryllus integer*), we compared the architecture of behavioural traits at the phenotypic and genetic level among five geographically separated populations of field crickets. Using a full-sib, half-sib breeding design, we recorded the activity, antipredator response, and boldness of 788 crickets from the five different populations. We detected the presence of an activity-antipredator response syndrome at the genetic level in two populations. However, matrix comparisons based on random skewer (all pairwise $r^{\circ} > 0.85$) and geometric subspace analyses (all p-values < 0.05) suggest that multivariate structure among behavioural traits were highly conserved among populations. This result was consistent at both genetic and phenotypic levels, suggesting also that environmental influences similarly affected different populations. Our results provide support for the constraints hypothesis and indicate that pleiotropy may strongly influence a populations' evolutionary responses.

Fixation probability in microbes – closing a 90 years gap of missing empirical data

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One of the most fundamental questions in population genetic theory addresses the fixation probability - the probability that the frequency of a particular allele in a population will reach 100 per cent. When a new allele arises in a population, it will initially be represented in very low numbers. This allele can be lost by genetic drift even when it is adaptive. Haldane's approximation (1927) states that the probability of fixation of a new beneficial allele is twice its fitness effect. This result has been generalised and extended by many authors in an overwhelming number of published models. However, empirical data of testing these predictions are scarce. Here, we use the bacterium Escherichia coli and the antibiotic-degrading enzyme TEM-1 -lactamase as a model system to test the probability that de novo beneficial (i.e. resistant) mutants will survive genetic drift and become

common. For this, a range of fluorescently labelled mutants (one to a few cells), resistant to the broad spectrum antibiotic cefotaxime (CTX), are introduced into a differently labelled wildtype population under various CTX concentrations, and cell ratios of both strains are determined after 48 hours. Experimental results are compared to predicted fixation probabilities based on mutant fitness estimates inferred from a discrete-time branching model (Schenk et al., 2012). By this, we aim on assessing to what extent short-term selection for antibiotic resistance can be predicted.

Epimutations in *C. elegans* mediated by small RNAs: rate, spectrum and long-term stability

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Epigenetic regulation of genes is essential for the development of multicellular organisms. In addition, it is becoming increasingly clear that some epigenetic changes in gene expression states can be transmitted transgenerationally, often remaining stable for several generations. As a result, there is much interest in the possibility that epigenetic changes can themselves contribute to evolutionary change in the absence of any changes in DNA sequence. However, this concept is controversial, with strong arguments both for and against a role for such "epimutations" in evolution. Here we use the nematode *C. elegans* as a model to provide the first detailed investigation of epimutations in animals. In *C. elegans*, long-term epigenetic silencing of transgenes has been shown to be mediated by small RNAs and the mechanism underlying their transgenerational transmission has been well described. We use mutation accumulation lines, grown for up to 400 generations under minimal selection, to investigate whether such silencing events occur at endogenous genes. We identify robust epimutations independent of DNA sequence changes, and estimate the rate at which they arise. Importantly however, we show that long-term longitudinal transmission of epimutations does not occur. Instead, epimutations occur at a fraction of genes which have intrinsically "noisy" levels of small RNAs, have a fast off-rate as well as on-rate and thus do not remain stable for multiple generations. We conclude that epimutations mediated by small RNAs are unlikely to contribute to evolutionary processes, at least under relatively stable environmental conditions.

Macroevolutionary consequences of gene flow during speciation

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Gene flow is predicted to affect the duration of speciation. Theoretical models predict that under its homogenizing effect, incipient species that manage to complete the speciation process must necessarily do so quickly, and that will result in a shorter duration of speciation. Therefore, gene flow has the potential to affect diversification dynamics and leave a signature in macroevolutionary patterns. The protracted birth-death model of diversification is a recent extension of birth-death model that incorporates the fact that speciation completion takes time and enables the inference of the duration of the speciation processes from phylogenetic trees. In this model, the extinction of incipient species can be alternatively interpreted as reabsorption via gene flow. The central prediction is that speciation duration estimated from phylogenetic trees will be shorter the higher the incidence of gene flow, also potentially affecting other diversification parameters inferred from molecular phylogenies. To address this question, we have conducted a comparative study using protracted birth-death species tree simulations along with multispecies coalescent gene tree simulations under different gene flow rate scenarios. Our results confirm this central prediction and illustrate how microevolutionary processes can impact macroevolutionary outcomes. Moreover, they suggest that studying the speciation duration from phylogenies have the potential to inform on the incidence of particular microevolutionary processes during the diversification of different groups of organisms.

AMR gene removal by conjugative delivery of CRISPR-Cas9

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Antimicrobial resistance (AMR) is a growing threat to healthcare: by 2050, AMR could cause more deaths than cancer worldwide. Many AMR-encoding genes are carried on accessory genetic elements like plasmids, which spread between phylogenetically distant members of bacterial communities. CRISPR-Cas based technologies may help combat the spread of AMR genes by removal of such plasmids. To optimise this technology, implementation of a delivery method which can reach a diverse range of bacteria is needed.

Therefore, we engineered broad host-range conjugative plasmid pKJK5 to express Cas9. pKJK5_Cas[GmR] expresses a guide RNA which targets Gentamycin resistance gene aacC1, while pKJK5_Cas[nt] expresses a non-targeting guide RNA. To confirm Cas9 activity on these plasmids, we electroporated *Escherichia coli* dh5 carrying either pKJK5_Cas version with targeted plasmid pHERD30T. Cas9 stopped plasmid entry, reducing average

transformation efficiency from 13500 cfu/ml/µg in presence of pKJK5_Cas[nt] to 0 for pKJK5_Cas[GmR]. Transformation efficiency of the untargeted plasmid pHERD20T was not affected. Additionally, the two versions of pKJK5_Cas do not show a difference in conjugation efficiency to other *E. coli* strains. Next, we delivered pKJK5_Cas[GmR] to *E. coli* K12 carrying pHERD30T by conjugation. This reduced the proportion of Gentamycin-resistant recipients by 33% compared to a recipient population treated with pKJK5_Cas[nt].

This proof-of-concept experiment shows how an engineered broad host-range conjugative plasmid is an effective means of removing AMR-encoding plasmids and may be a viable approach to remove resistance genes from complex bacterial communities. To make this method more effective, community experiments as well as optimisation of Cas9 activity are needed.

Genotype influences pre and post-meiotic sperm senescence in *Drosophila melanogaster*

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Deterioration in sperm quality with age is a major cause of male infertility. However, the causes, mechanisms, and consequences of declining sperm quality with age remain very poorly understood. First, it is unclear how much of the reduction in male fertility is due to declining sperm quality associated to advanced male age, or decreases in sperm performance as sperm age within male storage organs. Second, the precise consequences of sperm aging for male reproductive success, and offspring fitness are unclear. Third, the extent to which genetic background affects fertility senescence has not been systematically addressed. Here, we used a panel of 16 isogenic *Drosophila melanogaster* lines to test for genetic variation in sperm viability (percentage of viable cells) senescence, while disentangling two possible sources of variation, male (pre-meiotic) and sperm (post-meiotic) aging and how both affect male fertility and offspring quality. Results indicated complex interactions between male age and sperm age affecting reproductive performance, and these tended to be genotype dependent.

Genetic correlations and trade-offs as pathways to adaptive radiation

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Summarising two dissertation chapters, I will discuss evidence for divergent natural selection in creating changes in additive genetic variance to promote rapid adaptive divergence and facilitate adaptive radiation.

Genetic correlations between traits can concentrate genetic variance into fewer phenotypic dimensions that can bias evolutionary trajectories along the axis of greatest genetic variance and away from optimal phenotypes, constraining the rate of evolution. If genetic correlations limit adaptation, rapid adaptive divergence between multiple contrasting environments may be difficult. However, if natural selection can overcome genetic constraints after colonizing of new environments, an increase in genetic variance in the direction of selection can accelerate adaptive divergence. Here, we explored adaptive divergence of an Australian native wildflower by first exploring how changes in additive genetic variance compared with changes in phenotype mean for four contrasting ecotypes. We found that changes in phenotype mean aligned with changes in genetic variance, and more specifically, with changes in the major axis of genetic variance. We then conducted extensive reciprocal transplants, which showed that divergent natural selection created fitness trade-offs among the four contrasting habitats. Overall, our results suggest that large differences in natural selection between recently colonized and contrasting habitats select environment-specific alleles, likely segregating at low frequency. The rise in frequency of these rare alleles alter the distribution of genetic variance underlying phenotypic traits, increasing the amount of genetic variance in the direction of natural selection and facilitating rapid adaptive divergence during an adaptive radiation.

The Role of Host Genetics in the LInk Between the Microbiome and Rheumatoid Arthritis

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Background: Rheumatoid arthritis (RA) is a chronic autoimmune disease, characterised by painful synovium inflammation, bony erosions, immune activation and the circulation of autoantibodies. The relatively low concordance rate between monozygotic twins, 20 - 30% contrasts with heritability estimates of 60%, indicating a substantive role of other risk factors in RA pathogenesis. There is established evidence that RA has an infective component to its aetiology. More recently, differences in the commensal microbiome in RA compared to controls have been identified. Other groups have shown that the gut

microbiome differs in those with new onset and established RA patients compared to controls. However, whether altered microbiome reflects predisposing host genetics - which are known to influence the microbiome, or is a truly causal part of arthritis aetiology, remains to be determined. The use of humans matched for genetics –twins discordant for disease, is a unique study design which allows us to tease apart the influence of host genetics on the microbiome and determine if changes in the microbiome seen in RA are on the causal pathway for disease.

Methods: 1) Analysis of the diversity and taxonomic alterations of the gut microbiome in twins discordant for RA within the TwinsUK cohort. 2) A polygenic risk score (PRS) for RA was calculated in participants without clinical disease, and assessed for association with measures of the microbiome diversity and composition, using mixed effects models.

Results: 1) Lower diversity was found in RA patients compared to healthy co-twins, this was driven by RA associated taxonomic changes. 2) Genetic risk for RA did not correlate with diversity or compositional measures.

Conclusions: Alterations in the microbiome are present in RA and may contribute to disease aetiology. RA specific changes are not confounded by genetics, and thus may present a feasible therapeutic target.

Convergent genetic evolution, and our ability to detect it, is contingent on demographic history in Trinidadian guppies.

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Whether replicated phenotypes arise in natural populations through convergent genetic changes is poorly understood, but should be dependent on a range of factors such as shared ancestry and demographic history. We investigated whether convergent genomic evolution has occurred in a classic example of phenotypic convergent evolution: the Trinidadian guppy. We studied three naturally-occurring pairs of high (HP) and low (LP) predation populations, with LP populations being independently derived from downstream HP populations in three separate rivers. In this system, low predation environments have repeatedly selected for longer life histories, behavioural changes, and increased male colouration.

We first employed simulations of populations diverging under contrasting demographic treatments to demonstrate that measures of divergence and their use in detecting convergent evolution are hindered by demography. Specifically, our results highlight that the informativeness of relative divergence measures (i.e. FST, ϖ) for selection are dependent on migration and population contractions, whilst absolute measures (i.e. DXY) are generally uninformative at short timescales. Additionally, our ability to obtain similar values for measures of divergence across different demographic treatments is limited to certain clusters, regardless of all treatments experiencing the same selection. We then used our results to contextualise empirical measures of population divergence

from whole genome sequencing data in our guppy populations. In this way, we highlight demographic histories for which measures of divergence should be more closely associated with selection, and that outliers across multiple measures may be artefacts of demography rather than stronger candidates.

Our results highlight the cautiousness required when dealing with populations differing in demographic histories when studying convergent evolution in the wild.

The giant duckweed as a model for studying adaptation-in-action in plants

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To characterize the genotype-phenotype-fitness maps under the manipulated environment (adaption-in-action) is essential for understanding the process of adaptive evolution. However, this is extremely challenging, in particular for plants, mainly due to lacking a model system, in which multi-generational fitness can be measured within a short timeframe, and genotypic and phenotypic changes can be directly measured and manipulated. Our recent work shows that the giant duckweed (*Spirodela polyrhiza*), one of the fastest growing angiosperms, is an exceptionally suitable system for studying the process of adaptation-in-action. This plant reproduces predominantly through asexual budding with duplication rates of 2-3 days and a large number of plants can be grown with limited space under controlled conditions. The genomic diversity assessed from world-wide distributed samples and spontaneous mutation rates measured under natural conditions in this plant are low, which is ideal for investigating the process of adaptation from standing genetic variations. Furthermore, the rich microbiomes associated with this plant provide a unique opportunity for us to investigate the evolution of extended phenotypes in plants. With established tools of genetic manipulation in this plant, we will be able to further evaluate the adaptive value of the observed phenotypic and genotypic changes.

The pervasive population genomic impacts of genome duplication, gene flow, and selection

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The outcrossing relatives *Arabidopsis arenosa* and *Arabidopsis lyrata* are increasingly the subjects of population genomic studies of adaptive evolution. These works provide case studies for how population genomics can be applied to targeted questions, from understanding the basis of adaptation to whole genome duplication (WGD) to the genomic basis of adaptation to extreme environments, including toxic mines and high salinity soils. I present an overview of our studies that allows for a large-scale investigation of within- and between-population evolutionary dynamics in this model genus.

We individually resequenced ~600 *A. arenosa* genomes from 70 diploid and autopolyploid populations, allowing the dating and ordering of successive selective sweeps as lineages follow distinct evolutionary trajectories and diversify across Europe. We integrate these data with 120 *A. lyrata* and *Arabidopsis halleri* genomes for a genus-wide view of the genomic basis of diverse adaptations. In *A. arenosa*, we observe that the population genomic consequences of WGD are pervasive: following WGD there is evidence of a reduced efficacy of purifying selection, with an increase in non-synonymous polymorphisms, and patterns of linkage disequilibrium differ dramatically between ploidies. Autotetraploid diversity is further enriched via local introgression from distantly related diploid populations to the extent that the signal of tetraploid monophyly is largely erased, except at discrete loci resistant to interploidy introgression. Examples of such barrier loci encode alleles that mediate adaptation to WGD. In addition, the tetraploids specifically exchange compelling candidate alleles for interspecies adaptive gene flow with autotetraploid *A. lyrata*. We hypothesise that the combined effects of initial masking of deleterious mutations, a higher proportion of adaptive substitutions and rampant interploidy (and interspecies) introgression likely all conspire to shape the evolutionary potential of these young autopolyploids.

Cryptic evolution in Trinidadian guppies: A tale of two methods.

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Common garden experiments, in which population samples from before and after selection are reared under identical conditions, are considered the "gold standard" for demonstrating evolutionary change in natural populations. However, for many study species, it is not feasible to perform such experiments. Instead, many studies of evolution in wild populations have focussed on using mixed effects models structured with a relatedness matrix ('animal models') to estimate quantitative genetic parameters from long-term mark-recapture data. Estimates of evolutionary change from these studies can rarely be verified by independent methods. In this study, we use data from a long-term mark-recapture experiment, in which Trinidadian guppies from a population subject to intense predation pressure were introduced to a closed stretch of previously guppy-free, low-predation risk stream in the Northern Range tropical rainforest of Trinidad. This experimental introduction replicates the upstream invasion of guppies from regions of high- to low-predation risk, that has occurred naturally in multiple stream and river systems in Trinidad. In addition to intensive monthly mark-recapture work, juvenile guppies have been sampled from the introduction and ancestral source population each year, and reared for two generations under common garden conditions. We have used phenotypic and genetic data from this wild population to estimate quantitative genetic parameters using animal models. We focus on two traits: male size at maturity, and juvenile growth rate. Common garden data show that male size at maturity has increased over time relative to the ancestral population, whilst juvenile growth rate has not changed. This system therefore provides us with a unique opportunity to compare quantitative genetic estimates of evolutionary change with observations from common garden experiments, performed on individuals from the same wild population.

Multi-dimensional GWAS of aggregation behaviour in 200 *C. elegans* wild isolates

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The nematode worm *C. elegans* has been observed to aggregate into groups on food, and a mutation in a single neuropeptide receptor could switch animals from social to solitary (de Bono & Bargmann, 1998). Wild isolates of *C. elegans* aggregate to different degrees, however the natural variation of this behaviour has not been well-characterised. Here we performed high-resolution imaging of the aggregation behaviour in 200 wild strains (*Caenorhabditis* elegans Natural Diversity Resource), followed by multi-worm tracking and multi-dimensional quantitative behavioural phenotyping. We further identified several putative quantitative trait loci that contribute to different aggregation sub-phenotypes through GWAS.

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