

Biology News

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Department of Plant Sciences
Department of Zoology

Liam Dolan

Head of Department of Plant Sciences

Trees loom large in the highlights of the Department this year

John Baker



Liam Dolan

John MacKay is the inaugural Wood Chair in Forest Science and joined the Department in October 2013. John has made enormous contributions to our understanding the genetic diversity of conifers and was one of the lead authors on the publication that reported the genome sequence of the Norway Spruce. John's appointment

represents a commitment by the Department and University to forest science and has been enabled by the kind generosity of Sir Martin and Lady Audrey Wood, and the Patsy Wood Trust.

David Boshier was central to the development of "A Future with Broadleaved Trees", a strategy for the improvement of broadleaved trees in Britain and Ireland until 2035. This represents the first comprehensive attempt to develop an integrated strategy for the delivery of resources required to conserve and develop broad leaved trees in the face of invasive diseases and climate change. It builds on the local collaboration with the Earth Trust, which is based at Little Wittenham, and founded by ex-members of the Department more than 30 years ago.

As part of the assessment of research in UK universities (Research Excellence Framework) the Department submitted an Impact Case based on William Hawthorne's groundbreaking research on forest biodiversity. William has been on a campaign to map and rate centres of biological diversity around the world. As part of this program he has developed new protocols for efficiently surveying diversity that

allow policy makers to prioritise species and regions of forest for conservation. Adoption of his recommendations in Ghana have been the basis for laws enacted in the late 1990s to protect the sustainability of forestry activities and underpinned the adoption of a bilateral agreement for the licensing of timber for export from Ghana to the European Union which came into effect in 2013. This demonstrates the contribution of scientific knowledge to the development of policies that can safeguard forests for future generations.

Trees will be an important part of the future of the Department. We look forward to developing this theme with the collaboration of our extensive network of partners.

As we were going to press, we were very saddened by news of the death of Professor Lorna Casselton, who had been Foreign Secretary and Vice President of the Royal Society until 2011 and taught first year genetics practicals until a few weeks before her death. Lorna wrote an article for *Biology News* outlining some of her contributions to fungal genetics and it can be found on page 6.

Graduate student projects

Diversity in hotspots

Cicely Marshall (Merton College)

William Hawthorn



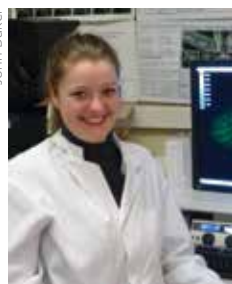
The world's rarest plant species are not distributed evenly around the world, but are found aggregated in regions called hotspots. While hotspots are relatively well

characterised at the species level, we know little about their genetic signatures. My research examines genetic diversity in hotspots to ask whether hotspots are promoting novel lineage diversity. I am building community phylogenies and species haplotype maps for hotspots in West Africa to ask what contribution recent lineage diversification has made to the biodiversity patterns we observe. Are hotspots also hotbeds of genetic innovation, or is their high endemism due to harbouring relictual lineages now extinct elsewhere?

Cell geometry and morphogenesis

Charlotte Kirchelle (St Cross College)

John Baker



Plant cells are fixed in their relative position in the tissue by their surrounding rigid cell wall, and cells in organ primordia have striking polyhedral geometries.

Changes in cell geometry and growth have to be coordinated to give rise to organs of defined shape. RAB-A5c is a regulatory component involved in membrane trafficking and identifies geometric edges of cells as distinct spatial domains with an apparent function in cell geometry control. Using a combination of 4D imaging, genetic, biochemical and biophysical techniques, I am testing the hypothesis that RAB-A5c acts through controlling the mechanical properties of cellular edges.

Trypanosome pathogens of plants

Eleanor Jaskowska (Keble College)

Olga Sedelnikova Baker



Trypanosomatids are a monophyletic group of unicellular eukaryotes, found in both free-living and parasitic forms. Evolved from a common ancestor, species of trypanosomatid

cause pathologies in hosts from crocodiles to cassava. Despite being discovered in plants over 100 years ago we know almost nothing about their biology. My research is focused on parasite cell surface proteins which interact with plant host immune system. Aside from improving our knowledge of how these pathogens interact with host crops such as coffee and palm oil, we might also uncover new clues as to how the ancestral trypanosomatid surface has been adapted to exploit different host environments.

Peter Holland

Head of Department of Zoology

Does Zoology have ‘impact’?



Peter Holland

One word that is never far from the agenda today is ‘impact’. Increasingly, Universities are being challenged to demonstrate that research, especially if funded from public funds (Research Councils and HEFCE), is having positive effects on the health, wealth, or well-being of people and the planet.

We will always argue that fundamental curiosity-driven research is essential, partly since surely it is important (and interesting!) to understand how the world works, but also because some far-reaching impacts come in quite unexpected ways. Recently, we reviewed the ‘impacts’ that have come from research in the Department of Zoology, and I think you will agree that the diversity is impressive. For example, Luke Alphey’s research showed how genetic modification could be applied to engineer sterile insects for the fight against mosquito-borne diseases; a spin-out company (Oxitec) was formed to develop the idea, and the method is in trials in Brazil and the Cayman Islands. Simon Hay’s work creates risk maps for malaria and other diseases, which governments and agencies use extensively. Oliver Pybus and colleagues developed methods for tracking and predicting the transmission and evolution of pathogens; these became part of the official UK response to the 2009 H1N1 ‘Swine Flu’ pandemic and are used extensively in other countries too. In the conservation arena, Jeremy Thomas’ ecological work has secured

the future of the Large Blue butterfly in the UK, Alex Rogers’ group has made major strides in assessing risk to threatened deep-sea habitats, and – amongst the success stories from our Wildlife Conservation Research Unit – Claudio Sillero and David Macdonald developed a novel rabies vaccination strategy that is safeguarding the Ethiopian wolf. In animal welfare, Marian Dawkins’ research has transformed the welfare of commercially-reared poultry and influenced EU Directives and industry practice (and was recognised by a well-deserved CBE in the 2014 New Years’ Honours). Most surprisingly of all, who would have predicted that software technology underpinning blockbuster computer games such as *Star Wars: The Force Unleashed* and *Clumsy Ninja* stemmed from animal movement research in the Department of Zoology? These are just a few examples, and there is much more to come, but hopefully even this snapshot shows that funding research in Zoology, and training the next generation of Biological Science undergraduates, really can have impact.

Graduate student projects

Octocoral communities of Mesoamerican Caribbean reefs

Vanessa Lovenburg (New College)

Jenny Murray



Coral reefs are under threat from anthropogenic and natural forces such as climate change, bleaching events, coral disease, over-fishing, coastal develop-

ment and eutrophication. Conservation monitoring and systematic understanding is essential to inform policy makers for the development of sustainable fisheries, marine protected areas, and predictive models for the future of the world’s oceans. I am studying the morphological and molecular diversity of octocoral communities (soft corals and gorgonians) on the Mesoamerican Barrier Reef System. My fieldwork is carried out with Operation Wallacea on the Honduran Bay Island of Utila.

Conservation of the Persian leopard

Mohammad Farhadinia (Lady Margaret Hall)

Mohammad Taghdolisi



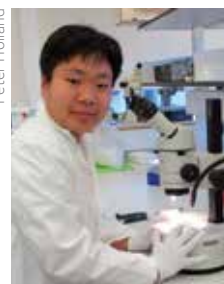
The Persian leopard is the largest cat in west Asia, and is considered to be endangered – poaching and habitat degradation are thought to be responsible. The rolling mountains

and high altitudes it favours present considerable challenges for scientists, and it is consequently one of the least known subspecies. I am a DPhil student in the WildCRU (Department of Zoology) who has been trying to rectify this. I am exploring the fundamental ecology of the population of Persian leopards, and how these big cats interact with the humans who live alongside. I am using a variety of modern technology, including camera traps, to do this.

Evolution and developmental roles of microRNAs

Shan Quah (Merton College)

Peter Holland



MicroRNAs (very small RNA molecules that do not code for proteins) are known to regulate the activity of genes, and many play important roles in embryonic

development. If we can determine how microRNAs evolve, especially how new microRNAs arise in evolution, this will help us understand how development, and therefore adult morphology, evolves. Using next-generation DNA and RNA sequencing and functional assays in cell culture, I am researching the evolution and developmental roles of microRNAs in mammals and Lepidoptera, discovering new microRNAs and their functions. I am funded by an A*STAR NSS (PhD) Scholarship.

Navigation over land and sea

Many long-distance migrants return each summer to their nesting sites with pin-point accuracy after having travelled hundreds or even thousands of kilometres. Carrier pigeons can arrive home efficiently from distant locations having traversed terrain they have never visited before. Navigation has long fascinated biologists, but much still remains unknown about the sensory and cognitive basis of the maps and compasses that animals use to plot these extraordinary journeys.

In the early 2000s, our group became one of the first to use the unprecedented precision of miniature GPS tracking devices to study navigational strategies in free-flying birds. Using homing pigeons as our chief study species, we have since uncovered a suite of unexpected phenomena, many of them overturning decades of received wisdom about the control of avian navigation.

Pigeons rarely home directly “as the crow flies”. Instead they quickly settle on individually preferred, idiosyncratic homing routes, which are often inefficient, and which they faithfully repeat with little deviation – much like us taking a preferred route to work each day. Their

journeys become structured by prominent landscape features – roads, rivers, railway lines, villages, and even power stations – strongly suggesting control by sequences of local visual landmark memories. Nevertheless, despite this “pilotage” we are finding that birds continue to pay attention to their time-compensated sun compass as they orient across the familiar

landscape even on remarkably fine spatial scales.

Homing pigeons can be GPS-tracked with exquisite precision over short distances, but unravelling the truly staggering journeys of oceanic navigators requires additional techniques. Combining GPS, dive logger, immersion logger and geolocator



Zsuzsa Akos

Pigeon routes: Repeated homing flights of a pigeon, showing idiosyncratic route choice

Undergraduate student projects

Elemental defence and plant-mediated interactions between herbivore guilds
José Waterton (St Hugh's College)



Anon

Herbivores can improve the feeding performance of others. Hyperaccumulating plants sequester high concentrations of metals

in their tissues; the ‘elemental defence’ hypothesis proposes that these metals protect against herbivore attack. I examined the effect that hyperaccumulation had on such plant-mediated, facilitative interactions between herbivores. By using herbivore feeding experiments in the greenhouse, I found that aphids improve the feeding performance of Lepidoptera larvae on the hyperaccumulator *Noccaea caerulea*. This facilitative effect appeared reduced on high zinc treatments; therefore, further research is required to confirm whether this might be an added advantage of elemental defences.

Nitrogen assimilation in land plants
Rebecca Watkins (Somerville College)



Caroline Trude

I worked in Liam Dolan’s lab investigating the genetic basis of nitrogen assimilation in *Marchantia polymorpha*. The liverwort is interesting

to study because of its early diverging position in land plant phylogeny. I conducted genetic and size analysis of plants grown in different nutrient conditions, and ran a mutant screen growing approximately 65,000 transgenic plants on media containing chlorate. I identified three mutants that will now be used for further research into the genes responsible for nitrogen assimilation and utilisation. I found working alongside a large group of researchers and students really helped me challenge myself, especially at lab meetings to dissect each project.

The effects of disturbance on butterfly diversity on Buton island, Indonesia
Emma Crookenden (Pembroke College)



Edward Crookenden

I studied the effects of disturbance on butterflies in Sulawesi with Operation Wallacea. A modified Pollard walk method was used at varying levels of disturbance. Abundance and richness were

similar at different disturbance levels, but population composition varied significantly. Endemic butterfly trends were different to the observed for generalist species, and the importance of focusing research on species with the highest conservation value was highlighted. Fruit-baited traps were set to consider vertical stratification of populations. Stratification was evident, with a number of species new to the study found only in the canopy. This implies that certain species may be misrepresented in Pollard walk surveys.

Zsuzsa Ákos



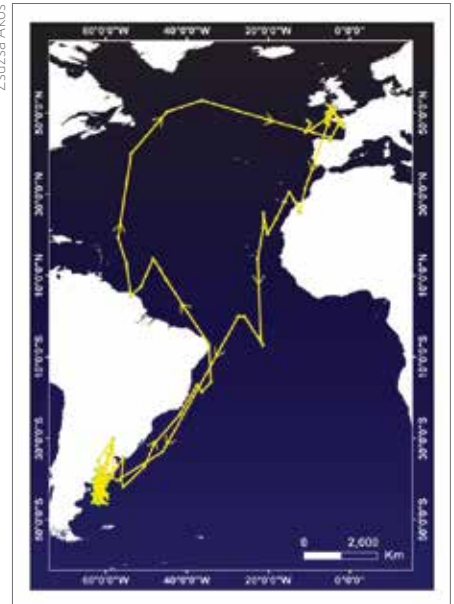
Homing pigeon carrying miniature GPS logger

data we have been tracking the foraging excursions and annual migration routes of the ocean-wandering seabirds (such as shearwaters and puffins) breeding on islands off Britain's western coasts. Novel machine learning techniques allow us to go beyond simply reconstructing routes, and pinpoint areas where birds stop-over to feed, dive, or rest – critical data for informing global marine conservation efforts. Tracking repeat individual migrations also shows us that, like pigeons, seabirds have individually idiosyncratic routes and destinations, confirming that the role of learning and memory extends to very long distance oceanic navigation too.

Recently, we have become interested in how birds make navigational decisions within groups. Birds in a flock travelling together face a problem that is ubiquitous among group-living species: how to resolve differences of opinion and remain cohesive. Humans can solve these problems democratically, by voting, or by appointing

leaders whom others follow. In collaboration with statistical physicists, and using high-resolution GPS data from flocks of pigeons, we have identified a subtle hierarchical arrangement that lies somewhere between democracy and despotism: each member of the flock can have some input into the navigational decisions of the flock, but some members' "votes" carry more weight than those of others. Interestingly, birds near the top of this leadership hierarchy are not necessarily more dominant socially, suggesting that hierarchies within the same collective are rearranged according to context. Why and how this happens – for example whether those best at navigating get to assume

Zsuzsa Ákos



Annual migration route of a Manx shearwater

leadership in flight – is the subject of our ongoing research aimed at understanding how evolution has shaped animals to deal with the challenges and opportunities that group living offers.

Dora Biro & Tim Guilford

Undergraduate student projects

Modelling the interaction between *Plasmodium falciparum* var genes and the human sickle cell trait

Susan Hawkins (St Catherine's College)

Barry Hawkins



My project was with Sunetra Gupta, where I studied the strain dynamics of malaria and its coevolutionary interactions with the human sickle cell allele. Through making

mathematical models, I discovered strain behaviours that had never been seen before, and it was the first time the effect of a haemoglobin disorder on malarial strain dynamics had ever been investigated. It was an enjoyable project to learn how to write models, and be the first to explore malaria and sickle cell coevolution in this way. I am now continuing this research as a DPhil student, through funding from the ERC and Clarendon Scholarship.

Molecular characterisation of the bacterial endosymbionts of two SWIR gastropods

Jack Howe (Hertford College)

Sally Le Page



The scaly-foot gastropod is found at deep-sea vents in the Indian Ocean. As

with other vent fauna, it is sustained by a bacterial endosymbiont that can harness the energetic chemistry of the vent-plumes. I investigated the symbiotic bacteria of this snail, alongside a second species novel to science, from a vent field near South Africa, to determine how they compared to each other and to species from other vents. Surprisingly, the novel snail harboured at least three distinct symbionts, and, while the scaly-foot gastropod contained only one symbiont, the bacteria showed some divergence to symbionts of this species collected from another site.

T-Cell receptor repertoire in T cell subsets during infection

Kirstie McLoughlin (Brasenose College)

Any Hong



My undergraduate dissertation investigated the relationship between T-cell clonality and function using T-cell receptor (TCR) repertoire analysis. I focused

on the relationship between regulatory and conventional T-cells using their TCR sequences to track distribution of clones in these subsets. The different T-cell subsets shared sequences (and thus clonal history) which indicated the potential for using TCR repertoire as a method to explore immune responses. I really enjoyed lab work, the success and the challenges, especially developing strong problem-solving skills that were needed to generate good data. The laboratory I worked in (Dr Adrian Smith's) was incredibly welcoming and supportive.

Gene homology – the key to tracing how sex evolved in fungi

John Baker



Coprinus spp, ink cap

One of the important themes of research in the Plant Sciences Department is how developmental pathways have evolved during land plant evolution. Over the last 25 years, the study of sex in multicellular fungi has also provided key insights into how evolution has tweaked gene function and regulation in response to the acquisition of different life styles and developmental complexity. Fungal sex genes were first identified in the unicellular budding yeast *Saccharomyces cerevisiae*, and this species was long considered a paradigm for understanding how they work, but in generating the mating type (*MAT*) locus,

evolution played an unexpected trick.

Filamentous ascomycete fungi such as the bread mould *Neurospora crassa*, and basidiomycete fungi such as the ink cap mushroom *Coprinus cinereus* have been favourite genetic tools for studying the eukaryotic cell for over 70 years. Ascomycetes and basidiomycetes form the Dikarya, a group in which most species are self-sterile

and must mate in order to complete their life cycle and produce sexual spores. Mating is achieved through action of the *MAT* locus with compatible mates having different genes at their *MAT* loci. The full complement of genes necessary for sexual development is only present when cells of the two mates fuse.

The name Dikarya derives from the fact that compatible cell fusion does not immediately lead to nuclear fusion. Instead there is a prolonged mycelial stage, known as the dikaryophase, in which the two different nuclei divide in synchrony in each

cell and are partitioned accurately by the formation of a clamp. In ascomycetes the dikaryophase is restricted within a short-lived fruiting body but in basidiomycetes it is the predominant stage and exists in the soil indefinitely, constantly giving rise to complex dikaryotic-celled fruiting bodies (to the delight of fungal foragers).

Long before gene cloning, it was recognised that genes at the *MAT* loci had essential roles in establishing and maintaining the dikaryophase. In unicellular basidiomycetes (such as the corn smut fungus *Ustilago maydis*) secreted pheromones are needed for mate recognition but in filamentous forms mate attraction has become superfluous and vegetative cell fusion is sufficient to determine whether mates are compatible. If fusion occurs, pheromone signalling is activated intracellularly to promote migration of the incoming nucleus. These same events (pheromone secretion, intracellular pheromone signalling, nuclear migration, clamp cell formation and fusion) can also clearly be seen in the development of ascomycete hyphae.

Given the shared developmental processes that occur during sex in both ascomycetes and basidiomycetes, and regulation in both groups by the *MAT* loci, it was long

Chickens on camera: health, welfare and efficient farming

People across the world want to eat more meat while livestock agriculture is under pressure to reduce greenhouse gas emissions and to use less water and land. Production, therefore, must become more efficient and more 'sustainably intensive'. But what does 'more efficient' mean for food animals themselves? Does more 'sustainably intensive' mean that pigs, chickens and cattle will have even less space, less food and less water than they have now? Is animal welfare on a collision course with human food security and tackling climate change?

Our research on the welfare of broiler (meat) chickens shows that such a clash is not inevitable and that, by working closely with commercial poultry

producers, more efficient farming may actually improve animal welfare. This is because some of the greatest improvements in both efficiency and welfare come from reducing mortality and waste and improving resistance to disease.

In collaboration with Stephen Roberts in the Department of Engineering Science, we are developing smartphone software to help farmers manage their flocks more effectively. The cameras on the phones monitor the movements of chicken flocks and the images are analyzed on the spot. The cameras do not track the movements of individual birds (that would be quite overwhelming in a house of 30,000 or more chickens) but each phone simply delivers a 4-number

description of its flock every 15 minutes. Remarkably, these four numbers allow us to detect flocks in which there is, or will be, a welfare issue. For example, flocks made up of healthy birds that walk easily can be distinguished from flocks containing a larger proportion of poor walkers with damaged legs and feet. The smartphones are able to predict these health problems in chicks as young as three days old, long before they show any clinical symptoms. We now want to know whether the smartphones can detect which flocks are carrying specific diseases. Working with Martin Maiden, Frances Colles and Adrian Smith in the Department of Zoology, we are looking at how our four indicator numbers vary with flocks with different levels and genotypes of *Campylobacter*, *Salmonella*, *Clostridium* and *Coccidia*.

Of course, a smartphone camera does not replace good human observation, but it does provide an extra eye for when

assumed that regulatory gene function first identified in the yeast *S. cerevisiae* would be conserved in other dikaryons. But evolution can be more sophisticated than that, and ascomycete and basidiomycete *MAT* loci harbour unrelated genes. In ascomycetes there are only two mating types (*a/alpha*, plus/minus) and one *MAT* locus; in its simplest form (found in filamentous ascomycetes) the two alternative forms of *MAT* contain different genes with one encoding an HMG-domain transcription factor and the other encoding an alpha-domain transcription factor. In combination, the two transcription factors induce the synthesis of mating type specific sex pheromones and of the corresponding receptors. Pheromones are secreted as attractants leading to fusion of compatible cells. This type of regulation works well when there are just two mating

types but in basidiomycetes there are thousands of mating types and as such the pheromone and other critical sex genes have to be regulated differently.

The essential genes for mate recognition and sexual development in basidiomycetes reside in two *MAT* loci. One locus contains the structural genes encoding different allelic forms of the all important sex pheromones and receptors and the other locus contains different allelic forms of a pair of homeodomain transcription factors (HD1 and HD2). Compatible cell fusion only occurs when different allelic forms of these HD proteins heterodimerise (HD1/HD2) to form a transcription factor unique to mated cells. Homologues of *HD1* and *HD2* genes have yet to be identified in filamentous ascomycetes but for such a conserved developmental pathway, evolution is unlikely to have invented other proteins to enable dikaryosis. Most likely the two genes encoding these proteins are another subset, along with the pheromone and receptor genes, that are regulated differentially in the two mating types by the HMG or alpha-domain transcription factors encoded at the *MAT* loci.

So how do these discoveries relate back to our understanding of sex in

unicellular yeasts where there is no dikaryophase because cell fusion is followed immediately by nuclear fusion? In the most ancient forms of the yeast *MAT* loci (as seen in *Candida albicans*), one locus has a gene encoding the typical ascomycete HMG-domain transcription factor linked to an *HD2* gene, and the other locus has a gene encoding the alpha-domain transcription factor linked to an *HD1* gene. Importantly there are telltale signs that these genes have been brought together by chromosome rearrangement. It is therefore hypothesised that the forms of *MAT* (*a* and *alpha*) that were first identified in *S. cerevisiae* were derived from an ancestral *HD1-HD2* gene pair. The *MAT a* locus retained the *HD2* gene and an inactivated *HD1* gene, while the *MAT alpha* locus retained the *HD1* gene and recombined with an alpha-domain transcription factor that replaced the *HD2* gene. The gene encoding the expected HMG domain transcription factor was lost from the *a* locus and so the pheromone and receptor genes it would have induced are now expressed constitutively and must be repressed in *MAT alpha* haploid cells, a new function for the *HD1* protein in addition to its function as a heterodimer in mated cells. Importantly this scenario could not have been envisaged without a comparative approach that focused on gene homology. Such approaches allow us to trace how evolution has adapted the tools at its disposal to promote new life styles and the developmental complexity that accompanies this.

Lorna A. Casselton

John Baker



Coprinus cinereus on petri dish

U.S. Department of Agriculture



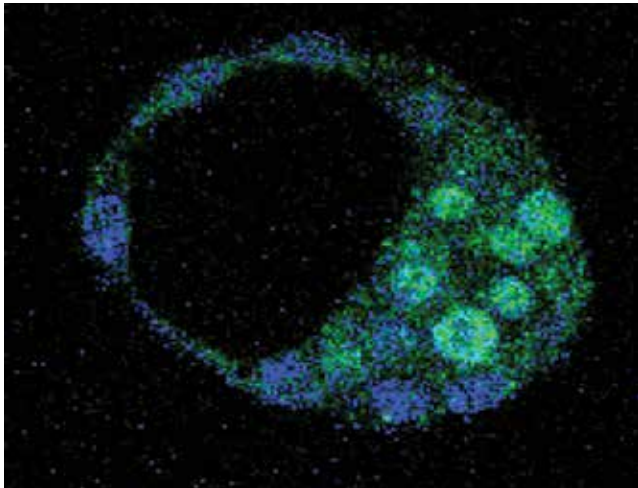
Most Broiler (meat) chickens are kept in large groups of up to 50,000 birds.

no-one can be present. Our ultimate aim is a phone app that farmers can carry around and then be warned when the cameras detect something unusual that would suggest an incipient health or welfare issue. Globally, 58 billion chickens are killed each year for food (nearly 1 billion in the UK), more individual animals than any other species. For the welfare of these animals to be taken seriously as part of the efficient farming of the future, welfare needs to be firmly linked to human food security, animal and human health and financial competitiveness. We hope that an easy to use smartphone app will go some way to forging these links and improving the lot of our commonest food animal.

Marian Stamp Dawkins

Mathematical ecology

Francesca Lock



Mouse blastocyst

Mathematical approaches play an ever-growing role in biology. Research work in the Department of Zoology has a rich history of the use and application of mathematical approaches. This tradition continues today, with research spanning the hierarchy of complexity in the life sciences. At the centre of our work is a desire to understand how diversity in life evolves and is organised; how do deterministic and perceivably more random processes interact to affect biological complexity?

Theoretical Developmental Biology

The organisation of early mammalian embryos is a venerable problem (and has had a research focus in Zoology for almost 50 years). For example, how do cells in the early embryo organize themselves, and does predetermined patterning exist? In work with Chris Graham (and colleagues from the Maths Institute in Oxford) we have shown how simple rule-based decisions of cell organisation can explain the increasing array of experimental patterns in early mammalian embryos. More recently, our theoretical models are being put to work (with colleagues at Southampton) to explore cell allocation decisions in the blastocyst (the ball of cells which is made up a group of 'inside' and a group of 'outside' cells). Allocation to outside cells (trophoblast) and inside cells (inner cell mass) is predicted to be controlled, amongst other things, by variability in cell cycle times between these two different groups of cells.

Evolution of Parental Care

How and why parental care evolved and how it is maintained draws on both evolutionary and ecological theory. Care is expected to increase offspring survival, be costly (in an evolutionary sense) to the

parent (or parents) but ensures a parent get its genes into future generations. However, parents often cannibalise offspring. Our theoretical work on the evolution of parental care (with Hope Klug at the University of Tennessee) emphasizes the ecological conditions under which care or cannibalism might evolve. Some key findings are that ecological resource competition plays an important role.

Care is more likely to evolve when adult life-spans are short: individuals have more to lose if their capacity to reproduce is curtailed, and parental investment in just increasing offspring survival through the vulnerable life stages can evolve as the only benefit of care (without any other benefits such as the need for sustained provisioning).

GM Insects

For almost 10 years now we have been working with Oxitec, a spin out company from Zoology, that has developed novel genetic-based technologies for the control insect pests and vectors. These technologies work very much like the sterile insect technique in aiming to reduce the size of pest (or vector) populations and, in recent field trials, Oxitec have proven achievements in the reduction of both agricultural pests and human disease vectors.

Allen Moore



Female burying beetle provisioning her larvae

Oxitec Ltd.



Aedes aegypti, the mosquito vector of dengue fever, taking a blood meal

Through competitive funding from BBSRC, we have recently completed a major project with Oxitec exploring the interface between insect ecology, genetics and GM technologies. A new BBSRC supported project with Oxitec and Imperial College aims to understand how these genetically-modified insects can be used to manage insect resistance. This work will focus on the diamondback moth which is a major pest of crucifer crops around the world. Conventional methods of control focus on the use of microbial and chemical pesticides yet diamondback moth has rapidly evolved resistance to these controls. Modelling work by Nina Alpey in the group has shown that the introduction of genetically-modified insects will not only reduce pest population size but should drive up susceptibility to conventional control methods by introgressing wildtype (not resistant) strains. The details matter and our new research project will build on this idea but also focus on specific applied issues like when and where is it optimal to undertake genetic-based methods of control to manage insect resistance.

The future

The future looks bright. Research in mathematical biology is highly collaborative, well placed to make conceptual and applied advances in the life sciences and as such it is really an exciting and vibrant time to be involved in this sort of research in Oxford.

Michael Bonsall

Paleovirology: ancient and modern viruses in animal genomes

Thomas Lersich



Chimpanzee, *Pan troglodytes*

The fossil record has contributed greatly to our understanding of the evolution of animal life. Viruses do not have such a physical fossil record as they do not persist for long outside an organism, and as a result, the long-term evolutionary biology of viruses has until recently been poorly understood. Another way to study evolution is to use analytical techniques to reconstruct evolutionary history from contemporary DNA sequence data. This approach is also limited when it comes to viruses, particularly for events that have occurred millions of years ago, because rapid rates of viral evolution erode the

information contained in DNA sequences. To circumvent these obstacles, we turn to the genomes of the organisms that viruses infect.

The genomes of animals are riddled with fragments of viruses that hold the key to understanding viral evolutionary history. They are known as endogenous viral elements (EVEs), and result from the integration of viral DNA into the genome of the hosts' reproductive cells. When this occurs, the virus is usually no longer functional, but its DNA can be passed on

to the offspring, behaving like any other host allele, capable of spreading within the population and potentially persisting for millions of years. Remarkably, EVEs that originate from retroviruses in humans make up approximately 5% of the genome, compared to only about 1.5% that codes for our own protein-coding genes.

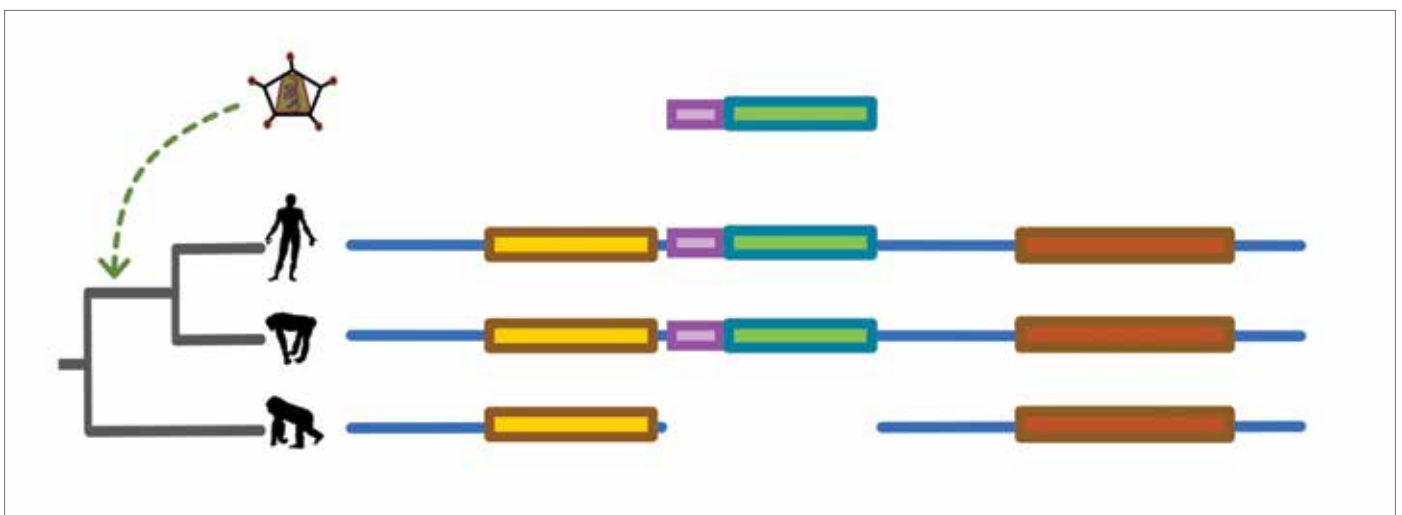
Once an EVE is formed, the rate of evolution of the viral sequence slows down by several orders of magnitude to the host neutral rate, preserving information about the virus' past for much longer. Retrovirus EVEs were identified in the late 1960s, and more recently we have demonstrated

that viruses of all known genome types and replication strategies can form EVEs. This includes viruses with DNA and RNA genomes, double and single stranded varieties of both forms, with dates of integration stretching back to the Cretaceous. This diverse set of ancient viral forms is a gold mine of evolutionary information, and is referred to as the 'viral fossil record'. The analysis of EVEs has greatly facilitated the study of viral evolution, and has led to the recently established field of palaeovirology.

Not all viruses in animal genomes are passive relics however. Occasionally endogenous retroviruses that are normally silent can be re-activated and this can have serious consequences for their host. A replicating retrovirus can reinsert into new genomic locations, potentially inactivating or altering the expression of a host gene. The inactivation of a tumour suppressor gene, for example, could lead to cancer. We know that some endogenous retroviruses can be more active in patients with several diseases such as cancer, autoimmune disorders or those with HIV/AIDS. However, it is currently unclear whether this upregulation is a cause or a consequence of disease. In collaboration with Gkikas Magiorkinis, we are looking into the nature of the upregulation of endogenous retroviruses in human disease in order to shed light on this connection, potentially leading to novel therapy targets in future.

Aris Katzourakis

Amr Aswad



An endogenous viral element that integrated in the common ancestor of chimpanzees and humans, but not orangutans. Coloured blocks indicate genes – viral genes are in green and purple.

Inbreeding modifies species interactions

Anne Muola



Abrostola asclepiadis feeding on *Vincetoxicum hirundinaria* (left)
Investigating the impact of inbreeding in a greenhouse experiment (right)

Today many plant species occur in small and fragmented populations where individuals mate with relatives or in extreme cases with themselves. This inbreeding has long been known to reduce plant fitness and population viability. More recently research has demonstrated that inbreeding can also influence the interactions between plants and other organisms by, for example, resulting in lower resistance to herbivores. This research has, however, been unrealistic in ignoring the impact of fragmentation on interacting species. In nature populations and communities of interacting species often decline together, especially if the interactions are very specialized. In interactions between insect herbivores and long-lived host plants herbivore populations are

likely to fluctuate more than host-plant populations, but they are also likely to be more connected due to migration between populations. A small plant population is not necessarily always associated with a small herbivore population and vice versa. This means that plants in inbred populations can interact with inbred or outbred herbivores, which can hugely influence how inbreeding affects their interactions.

For over a decade my research group has investigated the interactions between the long-lived perennial Swallow-wort (*Vincetoxicum hirundinaria*) and its specialist insect herbivores in a naturally fragmented archipelago landscape in SW Finland. We have been particularly interested in understanding how fragmentation influences the evolution or coevolution of these interactions. Our research has been motivated by the idea that understanding how fragmentation affects coevolution, a process responsible for creating and maintaining diversity, improves our ability to understand and predict its impact on diversity. Recently Aino Kalske, a PhD student in the group, wanted to understand better how inbreeding influences the interaction between the Swallow-wort and the leaf feeding specialist *Abrostola asclepiadis* depending on the level of inbreeding or outbreeding in both of the interacting species and not only in one of the species as had been done in previous studies.

In line with previous findings this research demonstrates that inbreeding reduces plant resistance to herbivores: inbred plants were consumed more and inbreeding also altered the defensive chemistry in the leaves. This negative effect of inbreeding on resistance was, however, reduced when inbred plants were eaten by inbred herbivores. Outbred herbivores were, in turn, able to take advantage of the altered chemistry and nutrient content in inbred plants and, therefore, outbred herbivores were able to consume more of the inbred plants. In other words, negative effects of inbreeding on plant resistance were more prominent when herbivores were outbred. When investigating the impact of herbivore inbreeding on their performance we found that inbreeding resulted in reduced performance, but that this inbreeding depression was more pronounced when herbivores were fed on inbred plants that are likely to be of poorer quality and, thus, a more stressful environment for the herbivores. Inbreeding depression is generally greater under stressful environments. This research provides the first evidence showing that the impact of inbreeding on traits central for species interactions depends on the level of inbreeding in both of the interacting species. Focusing on the effects of inbreeding on only one species at a time is likely to provide an unrealistic picture of its impact.

Roosa Leimu

From spiders' silks to medical devices

The spider's web is a marvel of engineering: gossamer threads combine to form a structure that can barely be seen, only glimpsed, but that nevertheless can stop (and hold) a bumblebee in full flight. In the web of the garden cross spider the mechanisms involved range from, self-assembling micro-scale windlasses and electrostatic charging in glue droplets, to nano-scale molecular arrangements.

As we all know, the threads of spider webs are silks. Not identical, but also not very different from the silks made by the mulberry silkworm used in commercial textiles. But because of the way they are spun, the silks of spiders are more easily studied than those of silkworms, and they have opened the door to new insights into the truly remarkable properties of all silks. Importantly, silk research provides a truly trans-disciplinary field for it requires

comprehensive biological understanding as well as the application of the fullest possible range of state-of-the-art tools and techniques developed in the polymer sciences.

In silks, water is the solvent and long-chain proteins are the main structural components. Protein and water molecules are interlaced in such a way that they can easily separate during 'spinning'. This dehydration denaturation ushers the protein molecules to refold, combine and interlink into a very tough and lasting material. Some spider silks, such as the frame and radial threads of a typical orb web, demonstrate the superb mechanical performance that can be achieved with this process. Molecular order, or rather the combination of ordered and disordered regions, determines strength and stretchiness. And exquisite spinning technology guarantees

Fritz Vollrath



Web of a sector spider, *Zygiella x-notata*, Oxford

Plants delivered by UPS

In plants, photosynthesis takes place within subcellular structures (organelles) called chloroplasts. A photosynthetic leaf cell typically contains ~100 chloroplasts, each one approximately 5 micrometres in diameter. Chloroplasts contain large quantities of the green pigment chlorophyll, which enables light absorption for photosynthesis, and as many as 3000 different types of protein. Although chloroplasts retain a functional genome of their own (an indicator of their evolutionary origin as free-living photosynthetic bacteria), the vast majority of chloroplast proteins are encoded in the nucleus and synthesized in the cytosol. These nucleus-encoded proteins must then be imported by chloroplasts, and this is achieved by sophisticated import machinery in the envelope membranes that surround each organelle.

Using a genetic screening approach, we recently identified a new gene called *SP1* that regulates the chloroplast protein import machinery. The *SP1* gene encodes a type of enzyme (a ubiquitin E3 ligase) that targets unwanted proteins for proteolytic removal by the cytosolic ubiquitin-proteasome system (UPS) – a major proteolytic system in eukaryotes that had not previously been linked to chloroplast development. The *SP1* protein is embedded in the outer envelope membrane of chloroplasts, where it acts to specifically control the abundance of key components of the protein import machinery. In this way, *SP1* is able

flawless filaments ranging in thickness from a few microns to a few tens of nanometers.

Fundamentally, moth silks are all of one basic design-type, while spider silks cover a wide range of types. Moreover, a silkmoth larva has only one set of glands while a spider produces several and rather different silk types each originating in a dedicated gland. Importantly, the ability to collect the silk under highly controlled conditions makes some spider silks excellent model materials in the pursuit of understanding animal silks. And there are important lessons to be learned, as we are finding out, about potentially transformational manufacturing technology for tough, sustainable, bio-inspired polymers fit for 21st century applications.

There are also novel applications for the silks themselves. An interesting feature of some silks is the excellent

Qihua Ling & Paul Jarvis



Images, taken using a transmission electron microscope, of typical chloroplasts in three different genotypes of *Arabidopsis thaliana*, superimposed on a photograph showing the appearance of the corresponding plants. Mutant plants with defects in chloroplast protein import (bottom) are considerably smaller and paler than wild-type plants (top). Differences in chloroplast development between the genotypes at the bottom left and bottom right are entirely due to altered activity of the *SP1* gene.

to regulate which proteins are imported by chloroplasts. Because imported proteins define the organellar proteome to a large extent, and are largely responsible for the functions of chloroplasts, *SP1* is very influential.

bio-compatibility combined with resorption in the human body. Some silks integrate faster into the body than others and this feature can be modified chemically in order to tune a medical device, for example. Silk threads can also be rendered chemically down to their molecules and then rebuild into forms other than threads. In this way one of our spin-out (so sorry) companies has developed a silk-based meniscal implant, hard and tough and with sponge-like holes to accommodate cell ingrowth. Funded largely by the Wellcome Trust, this implant is about to go into clinical trials. If successful, then this would be the first silk-based medical device on the market, other than, of course, the age-old silk suture threads still going strong. However this may be, the hopes for silks in regenerative medicine are very high all round.

Fritz Vollrath

Actually, chloroplasts are just one member of a broader family of structurally and functionally diverse organelles called plastids; other family members are etioplasts in dark-grown plants, chromoplasts in ripe fruit and flowers, and amyloplasts in roots, tubers and seeds. Different plastid types interconvert in response to developmental and environmental cues. For example, etioplasts quickly differentiate into chloroplasts as etiolated seedlings emerge into the light, to enable rapid photosynthetic establishment. During fruit ripening in tomato, bell pepper and citrus, chloroplasts transform into chromoplasts that synthesize and accumulate red, orange or yellow carotenoid pigments (which have dietary significance as provitamin A and as antioxidants). These plastid type interconversions are linked to reorganization of the organellar proteome, a process in which we believe *SP1* plays a critical role.

We have shown that *SP1* (which orchestrates UPS activity) is essential for chloroplast development from etioplasts in seedlings of the model plant *Arabidopsis thaliana* (thale cress); in fact, mutant plants lacking *SP1* are unable to de-etiolate efficiently, and die as a result. We believe that *SP1* will prove to be important during other developmental processes underpinned by plastid type interconversions, and, therefore, that *SP1* will find applications in crops. For example, by manipulating the activity of the *SP1* gene, it may be possible to speed up or slow down fruit ripening; doing so might help to prolong the shelf-life of certain fruits, reducing waste, or enable farmers to expedite ripening when time is limiting. Alternatively, the *SP1* technology may enable modification of amyloplast development in the grain of field crops such as wheat and rice, or alteration of the rate at which leaves age (a process characterized by the degeneration of chloroplasts into gerontoplasts), keeping crops green for longer and potentially improving yields. These and other exciting possibilities for the practical application of our research in crops are currently being investigated.

Paul Jarvis

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SATURDAY 20TH SEPTEMBER 2014
12.30 PM TO 5.00 PM

Attractions will include

TALKS:

Prof Phil Poole – ‘Addressing the Global Nitrogen Crisis’

Dr Lindsay Turnbull – ‘Looking Up and Looking Down: How to
Integrate Ecology into the Rest of Biology’

Prof Peter Holland – ‘Ecology, Evolution & Eccentricity:
A History of Zoology at Oxford’

Dr Ashleigh Griffin – ‘Evolutionary Biology: From Birds to Bacteria’

TOURS AND DISPLAYS:

Oxford University Herbaria, Department of Plant Sciences
Research & Teaching Exhibits, Department of Zoology

Refreshments will be served

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